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(54) **Primers for synthesising full-length cDNA and their use**

(57) Primers for synthesizing full-length cDNAs and their use are provided.

5602 cDNA encoding a human protein has been isolated and nucleotide sequences of 5'-, and 3'-ends of the cDNA have been determined. Furthermore, prim-

ers for synthesizing the full-length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full-length cDNA of the present invention containing the translation start site provides information useful for analyzing the functions of the protein.

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Description**FIELD OF THE INVENTION**

- 5 **[0001]** The present invention relates to a polynucleotide encoding a novel protein, a protein encoded by the polynucleotide, and new uses of these.

BACKGROUND OF THE INVENTION

- 10 **[0002]** Currently, the sequencing projects, the determination and analysis of the genomic DNA of various living organisms have been in progress all over the world. The whole genomic sequences of more than 10 species of prokaryotes, a lower eukaryote, yeast, and a multicellular eukaryote, *C. elegans* are already determined. As to human genome, which is supposed to be composed of three thousand million base pairs, the world wide cooperative projects have been under way to analyze it, and the whole structure is predicted to be determined by the years 2002-2003. The aim of the determination of genomic sequence is to reveal the functions of all genes and their regulation and to understand living organisms as a network of interactions between genes, proteins, cells or individuals through deducing the information in a genome, which is a blueprint of the highly complicated living organisms. To understand living organisms by utilizing the genomic information from various species is not only important as an academic subject, but also socially significant from the viewpoint of industrial application.

- 20 **[0003]** However, determination of genomic sequences itself cannot identify the functions of all genes. For example, as for yeast, only the function of approximately half of the 6000 genes, which is predicted based on the genomic sequence, was able to be deduced. As for human, the number of the genes is predicted to be approximately one hundred thousand. Therefore, it is desirable to establish "a high throughput analysis system of the gene functions" which allows us to identify rapidly and efficiently the functions of vast amounts of the genes obtained by the genomic sequencing.

- 25 **[0004]** Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to predict correctly the structure of encoded protein solely based on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows us to identify the primary structure of the protein easily. In human cDNA research, to date, more than one million ESTs (Expression Sequence Tags) are publicly available, and the ESTs presumably cover not less than 80% of all human genes.

- 30 **[0005]** The information of ESTs is utilized for analyzing the structure of human genome, or for predicting the exons of genomic sequences or their expression profile. However, many human ESTs have been derived from proximal regions to the 3'-end of cDNA, and information around the 5'-end of mRNA is extremely little. Among these human cDNAs, the number of the corresponding mRNAs whose encoding protein sequences are deduced is approximately 7000, and further, the number of full-length therein is only 5500. Thus, even including cDNA registered as EST, the percentage of human cDNA obtained so far is estimated to be 10-15% of all the genes.

- 35 **[0006]** It is possible to identify the transcription start site of mRNA on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA that is contained in the cDNA, or in its regulation of expression at the translation stage. Also, since a full-length cDNA contains ATG, the translation start site, in the 5'-region, it can be translated into a protein in a correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA or to analyze biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of a full-length cDNA provides valuable information which complements the information from genome sequencing. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

- 40 **[0007]** Therefore, if a novel human full-length cDNA is isolated, it can be used for developing medicines for diseases in which the gene is involved. The protein encoded by the gene can be used as a drug by itself. Thus, it has great significance to obtain a full-length cDNA encoding a novel human protein.

- 45 **[0008]** In particular, human secretory proteins or membrane proteins would be useful by itself as a medicine like tissue plasminogen activator (TPA), or as a target of medicines like membrane receptors. In addition, genes for signal transduction-associated proteins (protein kinases, etc.), glycoprotein-associated proteins, transcription-associated proteins, etc. are genes whose relationships to human diseases have been elucidated. Moreover, genes for disease-associated proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

- 50 **[0009]** Therefore, it has great significance to isolate novel full-length cDNA clones of human, only few of which has been isolated. Especially, isolation of a novel cDNA clone encoding a secretory protein or membrane protein is desired since the protein itself would be useful as a medicine, and also the clones potentially include a gene associated with diseases. In addition, genes encoding proteins that are associated with signal transduction, glycoprotein, transcription, or diseases are expected to be useful as target molecules for therapy, or as medicines themselves. These genes form a gene group predicted to be strongly associated with diseases. Thus, identification of the full-length cDNA clones

encoding those proteins has great significance.

SUMMARY OF THE INVENTION

[0010] An objective of the present invention is to provide a polynucleotide encoding a novel protein, a protein encoded by said polynucleotide, and novel usages of these.

[0011] The inventors have developed a method for efficiently cloning a human full-length cDNA that is predicted by the ATGpr etc. to be a full-length cDNA clone, from a full-length-enriched cDNA library that is synthesized by the oligo-capping method. Then, the inventors determined the nucleotide sequence of the obtained cDNA clones from both 5'- and 3'- ends.

[0012] Furthermore, the inventors analyzed the obtained clones by the BLAST search of the databases, SwissProt (http://www.ebi.ac.uk/ebi_docs/SwissProt_db/swisshome.html), GenBank (<http://www.ncbi.nlm.nih.gov/web/GenBank>), and UniGene (Human) (<http://www.ncbi.nlm.nih.gov/UniGene>).

[0013] The full-length cDNA clones of the present invention have high fullness ratio since these were obtained by the combination of (1) construction of a full-length-enriched cDNA library that is synthesized by the oligo-capping method, and (2) a system in which the full-length ratio is evaluated from the nucleotide sequence of the 5'-end (selection based on the ATGpr, previously removed complete sequences to ESTs). However, the primer of the present invention enables to obtain full-length cDNA easily without any specialized methods as in the described method.

Homology analysis in which the analysis is carried out against a not-full-length cDNA fragment to postulate the function of a protein encoded by said fragment, is being commonly performed.

However, since such analysis is based on the information of the fragment, it is not clear as to whether this fragment corresponds to a part that is functionally important in the protein. In other words, the reliability of the homology analysis based on the information of a fragment is doubtful, as information related to the structure of the whole protein is not available. However, the homology analysis of the present invention is conducted based on the information of a full-length cDNA comprising the whole coding region of the cDNA, and therefore, the homology of various portions of the protein can be analyzed. Hence, the reliability of the homology analysis has been dramatically improved in the present invention.

[0014] The inventors completed the invention by finding that it is possible to synthesize a novel full-length cDNA by using the combination of a primer that is designed based on the nucleotide sequence of the 5'-ends of the selected full-length cDNA clones and any of an oligo-dT primer or a 3'-primer that is designed based on the nucleotide sequence of the 3'-ends of the selected clones.

[0015] Thus, the present invention relates to primers described below, a method for synthesizing a polynucleotide using the primers, and polynucleotides obtained by the method.

[0016] First, the present invention relates to

(1) use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides;

(2) a primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides; and

(3) a primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence / 3'-end nucleotide sequence is selected from the combinations of 5'-end nucleotide sequence / 3'-end nucleotide sequence set forth in the SEQ ID NOs in Tables 1 and 2.

[0017] Tables 1 and 2 shows names of clones obtained in the examples described later, comprising the polynucleotide of the present invention (Table 1; 5547 clones, Table 2; 54 clones), names of nucleotide sequences at the 5'-end and 3'-end of the full-length cDNA, and their corresponding SEQ ID NOs. A blank indicates that the 3'-end sequence corresponding to the 5'-end sequence has not been determined for the same clone.

[0018] The SEQ ID NO of a 5'-end sequence is shown on the right side of the name of the 5'-end sequence, and the SEQ ID NO of a 3'-end sequence is shown on the right side of the name of the 3'-end sequence.

Table 2

name of clone	name of 5'-end sequence	SEQ ID of 5'-end sequence	name of 3'-end sequence	SEQ ID of 3'-end sequence
HEMBA1000497	F-HEMBA1000497	16111	R-HEMBA1000497	16165
HEMBA1001750	F-HEMBA1001750	16112	R-HEMBA1001750	16166
HEMBA1003854	F-HEMBA1003854	16113	R-HEMBA1003854	16167
HEMBA1004193	F-HEMBA1004193	16114	R-HEMBA1004193	16168
HEMBA1004860	F-HEMBA1004860	16115	R-HEMBA1004860	16169
HEMBA1005572	F-HEMBA1005572	16116	R-HEMBA1005572	16170
HEMBA1006038	F-HEMBA1006038	16117	R-HEMBA1006038	16171
HEMBA1006092	F-HEMBA1006092	16118	R-HEMBA1006092	16172
HEMBA1006406	F-HEMBA1006406	16119	R-HEMBA1006406	16173
HEMBA1006650	F-HEMBA1006650	16120	R-HEMBA1006650	16174
HEMBA1006812	F-HEMBA1006812	16121	R-HEMBA1006812	16175
HEMBB1000672	F-HEMBB1000672	16122	R-HEMBB1000672	16176
HEMBB1001197	F-HEMBB1001197	16123	R-HEMBB1001197	16177
HEMBB1001871	F-HEMBB1001871	16124	R-HEMBB1001871	16178
MAMMA1001252	F-MAMMA1001252	16125	R-MAMMA1001252	16179
MAMMA1002094	F-MAMMA1002094	16126	R-MAMMA1002094	16180
NT2RM4000634	F-NT2RM4000634	16127	R-NT2RM4000634	16181
NT2RM4000657	F-NT2RM4000657	16128	R-NT2RM4000657	16182
NT2RM4000783	F-NT2RM4000783	16129	R-NT2RM4000783	16183
NT2RM4000857	F-NT2RM4000857	16130	R-NT2RM4000857	16184
NT2RM4001178	F-NT2RM4001178	16131	R-NT2RM4001178	16185
NT2RM4002420	F-NT2RM4002420	16132	R-NT2RM4002420	16186
NT2RP2000198	F-NT2RP2000198	16133	R-NT2RP2000198	16187
NT2RP2000551	F-NT2RP2000551	16134	R-NT2RP2000551	16188
NT2RP2000660	F-NT2RP2000660	16135	R-NT2RP2000660	16189

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	NT2RP2001214	F-NT2RP2001214	16136	R-NT2RP2001214	16190
	NT2RP2001460	F-NT2RP2001460	16137	R-NT2RP2001460	16191
5	NT2RP2001756	F-NT2RP2001756	16138	R-NT2RP2001756	16192
	NT2RP2002056	F-NT2RP2002056	16139	R-NT2RP2002056	16193
	NT2RP2002677	F-NT2RP2002677	16140	R-NT2RP2002677	16194
	NT2RP2002755	F-NT2RP2002755	16141	R-NT2RP2002755	16195
10	NT2RP2002843	F-NT2RP2002843	16142	R-NT2RP2002843	16196
	NT2RP2003101	F-NT2RP2003101	16143	R-NT2RP2003101	16197
	NT2RP2003799	F-NT2RP2003799	16144	R-NT2RP2003799	16198
	NT2RP2004095	F-NT2RP2004095	16145	R-NT2RP2004095	16199
15	NT2RP2004732	F-NT2RP2004732	16146	R-NT2RP2004732	16200
	NT2RP2004920	F-NT2RP2004920	16147	R-NT2RP2004920	16201
	NT2RP2005454	F-NT2RP2005454	16148	R-NT2RP2005454	16202
	NT2RP2005776	F-NT2RP2005776	16149	R-NT2RP2005776	16203
20	NT2RP2005806	F-NT2RP2005806	16150	R-NT2RP2005806	16204
	NT2RP2005882	F-NT2RP2005882	16151	R-NT2RP2005882	16205
	NT2RP3001282	F-NT2RP3001282	16152	R-NT2RP3001282	16206
25	NT2RP3001723	F-NT2RP3001723	16153	R-NT2RP3001723	16207
	NT2RP3002099	F-NT2RP3002099	16154	R-NT2RP3002099	16208
	NT2RP3003155	F-NT2RP3003155	16155	R-NT2RP3003155	16209
	NT2RP3004028	F-NT2RP3004028	16156	R-NT2RP3004028	16210
30	OVARC1000008	F-OVARC1000008	16157	R-OVARC1000008	16211
	OVARC1000724	F-OVARC1000724	16158	R-OVARC1000724	16212
	OVARC1000751	F-OVARC1000751	16159	R-OVARC1000751	16213
	OVARC1001029	F-OVARC1001029	16160	R-OVARC1001029	16214
35	PLACE1000814	F-PLACE1000814	16161	R-PLACE1000814	16215
	PLACE1003030	F-PLACE1003030	16162	R-PLACE1003030	16216
	PLACE1005549	F-PLACE1005549	16163	R-PLACE1005549	16217
40	PLACE1007218	F-PLACE1007218	16164	R-PLACE1007218	16218

[0019] Furthermore, the present invention relates to the use of the above primers, as described below.

- (4) A polynucleotide which can be synthesized with the primer set of (2) or (3).
- (5) A polynucleotide comprising a coding region in the polynucleotide of (4).
- (6) A substantially pure protein encoded by polynucleotide of (4).
- (7) A partial peptide of the protein of (6).

[0020] In addition, the present invention comprises a polynucleotide described below and a protein encoded by the polynucleotide.

- (8) An isolated polynucleotide selected from the group consisting of

- (a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351;
- (b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351;
- (c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence

selected from the amino acid sequences set forth in the SEQ ID NOs in Tables 350 and 351, in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences set forth in the SEQ ID NOs in Tables 350 and 351;

(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Tables 350 and 351, and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Tables 350 and 351;

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351.

(9) A substantially pure protein encoded by the polynucleotide of (8).

(10) An antibody against the protein or peptide of any one of (6), (7), and (9).

(11) A vector comprising the polynucleotide of (5) or (8).

(12) A transformant carrying the polynucleotide of (5) or (8), or the vector of (11).

(13) A transformant expressively carrying the polynucleotide of (5) or (8), or the vector of (11).

(14) A method for producing the protein or peptide of any one of (6), (7), and (9), comprising culturing the transformant of (13) and recovering the expression product.

(15) An oligonucleotide comprising the nucleotide sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351 or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

(16) Use of the oligonucleotide of (15) as a primer for synthesizing a polynucleotide.

(17) Use of the oligonucleotide of (15) as a probe for detecting a gene.

(18) An antisense polynucleotide against the polynucleotide of (8), or the portion thereof.

(19) A method for synthesizing a polynucleotide, the method comprising:

- a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of (2) or (3), or the primer of (16); and
- b) recovering the synthesized product.

(20) The method of (19), wherein the cDNA library is obtainable by oligo-capping method.

(21) The method of (19), wherein the complementary strand is obtainable by PCR.

(22) A method for detecting the polynucleotide of (8), the method comprising:

- a) incubating a target polynucleotide with the oligonucleotide of (15) under the conditions where hybridization occurs, and
- b) detecting the hybridization of the target polynucleotide with the oligonucleotide of (15).

(23) A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Tables 350 and 351 and/or the amino acid sequences set forth in the SEQ ID NOs in Tables 350 and 351, or a medium on which the database is stored.

[0021] Any patents, patent applications, and publications cited herein are incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] Figure 1 shows the restriction maps of vectors pME18SFL3 and pUC19FL3.

[0023] Figure 2 shows the reproducibility of gene expression analysis. The respective intensities of gene expression observed in independent set of experiments are plotted in the vertical axis as well as in the horizontal axis.

[0024] Figure 3 shows the detection limit in gene expression analysis. The intensity of expression is shown in the vertical axis and the concentration ($\mu\text{g/ml}$) of probe used is shown in the horizontal axis.

DETAILED DESCRIPTION OF THE INVENTION

[0025] Herein, "polynucleotide" is defined as a molecule in which multiple nucleotides are polymerized. There are no limitations in the number of the polymerized nucleotides. In case that the polymer contains relatively low number

of nucleotides, it is also described as an "oligonucleotide". The polynucleotide or the oligonucleotide of the present invention can be a natural or chemically synthesized product. Alternatively, it can be synthesized using a template DNA by an enzymatic reaction such as PCR.

[0026] All the cDNA provided by the invention are full-length cDNA. Herein, a "full-length cDNA" is defined as a cDNA which contains both ATG codon (the translation start site) and the stop codon. Accordingly, the untranslated regions, which are originally found in the upstream or downstream of the protein coding region in natural mRNA, may or may not be contained.

[0027] An "isolated polynucleotide" is a polynucleotide the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example,

(a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs;

(b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA;

(c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and

(d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein. Specifically excluded from this definition are nucleic acids present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones: e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0028] The term "substantially pure" as used herein in reference to a given polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. The substantially pure protein or polypeptide is at least 75% (e.g., at least 80, 85, 95, or 99%) pure by dry weight. Purity can be measured by any appropriate standard method, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

[0029] All the clones (5602 clones) of the present invention are novel and encode the full-length proteins. All the clones were prepared by oligo capping method, which can achieve cDNA cloning with high fullness ratio. The cDNA clones were selected by using ATGp1 score as an index of the fullness ratio at the 5'-end, based on the sequence features of the 5'-end sequences. Selection was further carried out by searching GenBank database for EST sequences homologous to 5'-end sequence of each clone by BLAST [S.F. Altschul, W. Gish, W. Miller, E.W. Myers & D.L. Lipman J. Mol. Biol., 215:403-410 (1990); W. Gish, & D.J. States, Nature Genet., 3:266-272 (1993)] and by considering the number of matching (identical) EST sequences or the number of continuous amino acids in the 5'-end sequence initiated from the initiation codon.

[0030] Moreover, the clones were turn out to be not identical to any of the known human mRNA (namely novel) by homology search using the 5'-end sequence.

[0031] The primers of the present invention, which are used for synthesizing full-length cDNA, are selected from the group comprising SEQ ID NO: 1-5547 (5'-primer), or SEQ ID NO: 5548-10463 (3'-primer). Further, the primers of the present invention, which are used for synthesizing full-length cDNA, are selected from SEQ ID NO: 16111-16164 (5'-primer), or SEQ ID NO: 16165-16218 (3'-primer). Some of the nucleotides include a known EST as its part. However, the primers of the present invention are novel in terms that the primers enable to synthesize full-length cDNA. Because the known ESTs lack important information on what part of cDNA the ESTs correspond to, it is impossible to design primers on the basis of the ESTs.

[0032] All the full-length cDNA of the present invention can be synthesized using a primer set comprising the nucleotide sequences selected from both the 5'-and 3'-end sequences, or a set comprising a primer based on the 5'-end sequence and an oligo-dT primer, by a method such as PCR (Current protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 6.1-6.4).

[0033] Specifically, PCR can be performed using an oligonucleotide that has 15 nucleotides longer, and specifically hybridizes with the complementary strand of the polynucleotide that contains the nucleotide sequence selected from the 5'-end sequences shown in Table 1 and 2 (SEQ ID NO: 1-5547, or SEQ ID NO: 16111-16164), and an oligo-dT primer as a 5'-, and 3'-primer, respectively. The length of the primers is usually 15-100 bp, and favorably between 15-35 bp. In case of LA PCR, which is described below, the primer length of 25-35 bp may provide a good result.

[0034] A method to design a primer that enables a specific amplification based on the given nucleotide sequence is known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In designing a primer based on the 5'-end sequence, the primer is designed so as that, in principle, the amplification products will include the translation start site. Accordingly, in case that a given 5'-end nucleotide sequence is the 5'- untranslated region (5'UTR), any part of the sequence can be used as a 5'-primer as far as the specificity toward the target cDNA is insured. The translation start site can be predicted using a known method such

as the ATGpr as described below.

[0035] When synthesizing a polynucleotide, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. However, it is possible to amplify such a long nucleotides by using such as LA PCR (Long and Accurate PCR). It is advantageous to use LA PCR when synthesizing long DNA. In LA PCR, in which a special DNA polymerase having 3' → 5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, it is reported that amplification of a nucleotide with 20 kb longer can be achieved under desirable condition (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

[0036] A template DNA for synthesizing the cDNA of the present invention can be obtained by using cDNA libraries that are prepared by various methods. The full-length cDNA clones obtained here are those with high fullness ratio, which were obtained using a combination of (1) a method to prepare a full-length-enriched cDNA library using the oligo-capping method, and (2) an estimation system for fullness using the 5'-end sequence (selection based on the estimation by the ATGpr after removing clones that are not-full-length compared to the ESTs). However, it is possible to easily obtain a full-length cDNA by using the primers that are provided by the present invention, not by the above described specialized method.

The problem with the cDNA libraries prepared by the known methods or commercially available is that mRNA contained in the libraries has very low fullness ratio. Thus, it is difficult to screen full-length cDNA clone directly from the library using ordinary cloning methods. The present invention has revealed a primer that is capable of synthesizing a full-length cDNA. If provided with primers, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to synthesize a full-length cDNA with more reliability.

[0037] The 5'-end sequence of the full-length cDNA clones of the invention can be used to isolate the regulatory element of transcription including the promoter on the genome. By the spring of the year 2000, a rough draft of the human genome (analysis of human genomic sequence with lower accuracy), which covers 90% of the genome, is planned to be accomplished, and by the year 2003, analysis of the entire human genomic sequence is going to be finished. However, it is hard to analyze with software the transcription start sites on the human genome, in which long introns exist. By contrast, it is easy to specify the transcription start site on the genomic sequence using the 5'-end sequence of the full-length cDNA clone, thus it is easy to obtain the genomic region involved in transcription regulation, which includes the promoter that is contained in the upstream of the transcription start site.

[0038] The full-length cDNAs cloned in the present invention are classified into 13 groups, based on the data such as ATGpr1 score, by which the fullness ratio can be evaluated. Specifically, the 13 groups consist of; the below-mentioned groups (1)-(3), containing 3690 clones (Table 9), and the group (12), containing 3 clones, wherein ATGpr1 (score defined in the ATGpr program) is higher than 0.3; and the below-mentioned groups (4)-(11), containing 1857 clones (Table 10), and the group (13), containing 52 clones, wherein, although ATGpr1 is 0.3 or less, the clones are judged to be full-length from various viewpoints. Names of the clones belonging to the groups (1)-(13) are as indicated in Examples or below.

(1) 1516 clones

Among the 3690 clones that have the maximal ATGpr1 score higher than 0.3, 1516 clones are novel full-length clones, in which at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST.

(2) 377 clones

Among the 3690, 377 clones are novel full-length clones, in which the number of human EST having identical sequence at both 5'- and 3'-ends is 1 to 5.

(3) 1797 clones

Among the 3690, 1797 clones are novel full-length clones, in which the number of human EST having identical sequence at the 5'-end is not more than 20 (except the clones described above).

(4) 453 clones

Among the 1857 clones in which the maximal ATGpr1 score is 0.3 or less, the following 453 clones are estimated to be novel full-length clones since the clones have the maximal score 0.3 or more in the ATGpr2, and at least either of the sequences of their 5'- and 3'-ends, or both are not identical to those of any human EST. The ATGpr2 score is determined by using the ATGpr program with neglecting the information of the frequency of the six nucleotides contained within the sequence between the ATG codon and the stop codon (the maximal length is 300 nucleotides from the ATG codon) (Salamo A.A., Nishikawa T., and Swindells M.B. (1998) Bioinformatics, 14: 384-390; <http://www.hri.co.jp/atgpr/>). The ATGpr program for calculating the ATGpr2 score is described as the

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ATGpr2 program in the followings.

(5) 24 clones

Among the 1857 clones, 24 clones are estimated to be full-length since their maximal ATGpr2 scores are higher than 0.3, and also novel, though they have low scores in ATGpr1 program, in which the number of the human EST having identical sequence at both 5'- and 3'-ends is 1 to 5.

(6) 65 clones

Among the 1857 clones, 65 clones are estimated to be full-length since, though they have low scores in both programs, ATGpr1 and ATGpr2, the scores are the maximum in comparison to those of the other clones in the same cluster (at least two clones). The clones are also novel, if at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST.

(7) 32 clones

Among the 1857 clones, 32 clones are estimated to be full-length since, though they have low scores in both programs, ATGpr1 and ATGpr2, the scores are the maximum in comparison to those of the other clones in the same cluster (at least two clones). The clones are also novel, if the number of the human EST having identical sequence at both 5'- and 3'-ends is 1 to 5.

(8) 36 clones

Among the 1857 clones, 36 clones are full-length, which were selected by assembling the sequences of the other clones or human EST, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST.

(9) 81 clones

Among the 1857 clones, 81 clones are full-length, which were selected by assembling the sequences of the other clones or human EST, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if the number of the human EST having identical sequence at the 5'-end is not more than 20 (other than the clones in which at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST).

(10) 938 clones

Among the 1857 clones, 938 clones are estimated to be full-length according to the fullness ratio shown in Table 4, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if at least the sequence of the 5'-end is not identical to those of any human EST.

(11) 228 clones

Among the 1857 clones, 228 clones are estimated to be full-length according to the fullness ratio shown in Table 7, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if at least the sequence of the 3'-end is not identical to those of any human EST.

(12) 3 clones

Three clones, HEMBA1006812, HEMBB1001871, and NT2RP3001282, whose maximal ATGpr1 values are higher than 0.3, are full-length and novel clones whose 5'-end sequences presumably contain a coding region which is initiated with ATG codon and which encodes 100 amino acids or more.

(13) 52 clones

The following 52 clones, which have maximal ATGpr1 values of 0.3 or less, are full-length with the fullness ratios shown in Table 4 although the fullness ratios are low:

HEMBA1000497,	HEMBA1001750,	HEMBA1003854,	HEMBA1004193,	HEMBA1004860,	HEMBA1005572,
HEMBA1006038,	HEMBA1006092,	HEMBA1006406,	HEMBA1006650,	HEMBA1006672,	HEMBA1001197,
MAMMA1001252,	MAMMA1002094,	NT2RM4000634,	NT2RM4000657,	NT2RM4000783,	NT2RM4000857,
NT2RM4001178,	NT2RM4002420,	NT2RP2000198,	NT2RP2000551,	NT2RP2000660,	NT2RP2001214,
NT2RP2001460,	NT2RP2001756,	NT2RP2002056,	NT2RP2002677,	NT2RP2002755,	NT2RP2002843,
NT2RP2003101,	NT2RP2003799,	NT2RP2004095,	NT2RP2004732,	NT2RP2004920,	NT2RP2005454,
NT2RP2005776,	NT2RP2005806,	NT2RP2005882,	NT2RP3001723,	NT2RP3002099,	NT2RP3003155,
NT2RP3004028,	OVARC1000008,	OVARC1000724,	OVARC1000751,	OVARC1001029,	PLACE1000814,

PLACE1003030, PLACE1005549, PLACE1007218, NT2RP4002298.

Moreover, the clones are novel clones whose 5' -end sequences presumably contain a coding region which is initiated with ATG codon and which encodes 50 amino acids or more. Among them, the following 20 clones is predicted to contain a coding region with 100 amino acids or more and should encode proteins:

HEMBA1000497, HEMBA1003854, HEMBA1004193, NT2RM4000657, NT2RM4001178, NT2RP2001756, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2004095, NT2RP2004920, NT2RP2005806, NT2RP3002099, NT2RP3003155, OVARC1000724, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218.

[0039] The protein encoded by the polynucleotide of the invention can be prepared as a recombinant protein or as a natural protein. For example, the recombinant protein can be prepared by inserting the polynucleotide encoding the protein of the invention into a vector, introducing the vector into an appropriate host cell and purifying the protein expressed within the transformed host cell, as described below. In contrast, the natural protein can be prepared, for example, by utilizing an affinity column to which an antibody against the protein of the invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 16.1-16.19) is attached. The antibody used for affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, in vitro translation (See, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing the protein of the invention.

[0040] Proteins functionally equivalent to the proteins of the present invention can be prepared based on the activities, which were clarified in the above-mentioned manner, of the proteins of the present invention. Using the biological activity possessed by the protein of the invention as an index, it is possible to verify whether or not a particular protein is functionally equivalent to the protein of the invention by examining whether or not the protein has said activity.

[0041] Proteins functionally equivalent to the proteins of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into an amino acid sequence of a protein (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5). Besides, such proteins can be generated by spontaneous mutations. The present invention comprises the proteins having one or more amino acids substitutions, deletions, insertions and/or additions in the amino acid sequences of the proteins of the present invention (Tables 350 and 351), as far as the proteins have the equivalent functions to those of the proteins identified in the present Examples described later.

[0042] There are no limitations in the number and sites of amino acid mutations, as far as the proteins maintain the functions thereof. The number of mutations is typically 30% or less, or 20% or less, or 10% or less, preferably within 5% or less, or 3% or less of the total amino acids, more preferably within 2% or less or 1 % or less of the total amino acids. From the viewpoint of maintaining the protein function, it is preferable that a substituted amino has a similar property to that of the original amino acid. For example, Ala, Val, Leu, Ile, Pro, Met, Phe and Trp are assumed to have similar properties to one another because they are all classified into a group of non-polar amino acids. Similarly, substitution can be performed among non-charged amino acid such as Gly, Ser, Thr, Cys, Tyr, Asn, and Gln, acidic amino acids such as Asp and Glu, and basic amino acids such as Lys, Arg, and His.

[0043] In addition, proteins functionally equivalent to the proteins of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using the hybridization technique (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a DNA highly homologous to the DNA encoding the protein identified in the present Example based on the identified nucleotide sequence (Tables 350 and 351) or a portion thereof and obtain the functionally equivalent protein from the isolated DNA. The present invention include proteins encoded by the DNAs hybridizing with the DNAs encoding the proteins identified in the present Example, as far as the proteins are functionally equivalent to the proteins identified in the present Example. Organisms from which the functionally equivalent proteins are isolated are illustrated by vertebrates such as human, mouse, rat, rabbit, pig and bovine, but are not limited to these animals.

[0044] Washing conditions of hybridization for the isolation of DNAs encoding the functionally equivalent proteins are usually "1 × SSC, 0.1% SDS, 37°C"; more stringent conditions are "0.5 × SSC, 0.1% SDS, 42°C"; and still more stringent conditions are "0.1 × SSC, 0.1% SDS, 65°C". Alternatively, the following conditions can be given as hybridization conditions of the present invention. Namely, conditions in which the hybridization is done at "6 × SSC, 40% Formamide, 25°C", and the washing at "1 × SSC, 55°C" can be given. More preferable conditions are those in which the hybridization is done at "6 × SSC, 40% Formamide, 37°C", and the washing at "0.2 × SSC, 55°C". Even more preferable are those in which the hybridization is done at "6 × SSC, 50% Formamide, 37°C", and the washing at "0.1 × SSC, 62°C". The more stringent the conditions of hybridization are, the more frequently the DNAs highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5 × SSC, 0.1% SDS, 42°C", or alternatively, hybridization conditions of "6 × SSC, 40% Formamide, 37°C", and the washing at "0.2 × SSC, 55°C". However, the above-mentioned combinations of SSC, SDS and temperature conditions are indicated just as examples.

Those skilled in the art can select the hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors (for example, probe concentration, probe length and duration of hybridization reaction) that determines the stringency of hybridization.

[0045] The amino acid sequences of proteins isolated by using the hybridization techniques usually exhibit high homology to those of the proteins of the present invention, which are shown in Tables 350 and 351. The present invention encompasses a polynucleotide comprising a nucleotide sequence that has a high identity to the nucleotide sequence of claim 8 (a).

Furthermore, the present invention encompasses a peptide, or protein comprising an amino acid sequence that has a high identity to the amino acid sequence encoded by the polynucleotide of claim 8 (b). The term "high identity" indicates sequence identity of at least 40% or more; preferably 60% or more; and more preferably 70% or more. Alternatively, more preferable is identity of 90% or more, or 93% or more, or 95% or more, furthermore, 97% or more, or 99% or more. The identity can be determined by using the BLAST search algorithm.

[0046] With the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)) using primers designed based on the nucleotide sequence (Tables 350 and 351) or a portion thereof identified in the present Example, it is possible to isolate a DNA fragment highly homologous to the polynucleotide sequence or a portion thereof and to obtain functionally equivalent protein to a particular protein identified in the present Example based on the isolated DNA fragment.

[0047] The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, score = 50, wordlength = 3. When gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) are used. See <http://www.ncbi.nlm.nih.gov>.

[0048] The present invention also includes a partial peptide of the proteins of the invention. The partial peptide comprises a protein generated as a result that a signal peptide has been removed from a secretory protein. If the protein of the present invention has an activity as a receptor or a ligand, the partial peptide may function as a competitive inhibitor of the protein and may bind to the receptor (or ligand). In addition, the present invention comprises an antigen peptide for raising antibodies. For the peptides to be specific for the protein of the invention, the peptides comprise at least 7 amino acids, preferably 8 amino acids or more, more preferably 9 amino acids or more, and even more preferably 10 amino acids or more. The peptide can be used for preparing antibodies against the protein of the invention, or competitive inhibitors of them, and also screening for a receptor that binds to the protein of the invention. The partial peptides of the invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or digesting the protein of the invention with an appropriate peptidase.

[0049] The present invention also relates to a vector into which the DNA of the invention is inserted. The vector of the invention is not limited as long as it contains the inserted DNA stably. For example, if *E. coli* is used as a host, vectors such as pBluescript vector (Stratagene) are preferable as a cloning vector. To produce the protein of the invention, expression vectors are especially useful. Any expression vector can be used as far as it is capable of expressing the protein *in vitro*, in *E. coli*, in cultured cells, or *in vivo*. For example, pBEST vector (Promega) is preferable for *in vitro* expression, pET vector (Invitrogen) for *E. coli*, pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8: 466-472) for *in vivo* expression. To insert the DNA of the invention, ligation utilizing restriction sites can be performed according to the standard method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0050] The present invention also relates to a transformant carrying the vector of the invention. Any cell can be used as a host into which the vector of the invention is inserted, and various kinds of host cells can be used depending on the purposes. For strong expression of the protein in eukaryotic cells, COS cells or CHO cells can be used, for example.

[0051] Introduction of the vector into host cells can be performed, for example, by calcium phosphate precipitation method, electroporation method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection method, etc.

[0052] The primer of the present invention can be used for synthesizing full-length cDNA, and also for the detection and/or diagnosis of the abnormality of the protein of the invention encoded by the full-length cDNA. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using the primer of the invention, DNA encoding the protein of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of the abnormality of the sequence by RFLP analysis, SSCP, or direct sequencing.

[0053] Furthermore, the "polynucleotide having a length of at least 15 nucleotides, comprising a nucleotide sequence that is complementary to a polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs in Tables 350 and 351, or its complementary strand" includes an antisense polynucleotide for suppressing the expression of the protein of the invention. To exert the antisense effect, the antisense polynucleotide has a length of at least 15 bp or more, for example, 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and has a length of usually 3000 bp or less and preferably 2000 bp or less. The antisense DNA can be used in the gene therapy of the diseases that are caused by the abnormality of the protein of the invention (abnormal function or abnormal expression). Said antisense DNA can be prepared, for example, by the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) *Nucleic Acids Res.* 16: 3209-3221) based on the nucleotide sequence of the DNA encoding the protein (for example, the DNA set forth in any one of SEQ ID NOs in Tables 350 and 351).

[0054] The polynucleotide or antisense DNA of the present invention can be used in gene therapy, for example, by administering it into a patient by the in vivo or ex vivo method with virus vectors such as retrovirus vectors, adenovirus vectors, and adeno-associated virus vectors, or non-virus vectors such as liposome.

[0055] The present invention also relates to antibodies that bind to the protein of the invention. There are no limitations in the form of the antibodies of the invention. They include polyclonal antibodies, monoclonal antibodies, or their portions that can bind to the protein of the invention. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies are also included.

[0056] The polyclonal antibody of the invention can be obtained according to the standard method by synthesizing an oligopeptide corresponding to the amino acid sequence and immunizing rabbits with the peptides (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.12-11.13). The monoclonal antibody of the invention can be obtained according to the standard method by purifying the protein expressed in *E. coli*, immunizing mice with the protein, and producing a hybridoma cell by fusing the spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 11.4-11.11).

[0057] The antibody binding to the protein of the present invention can be used for purification of the protein of the invention, and also for detection and/or diagnosis of the abnormalities of the expression and structure of the protein. Specifically, proteins can be extracted, for example, from tissues, blood, or cells; and the protein of the invention is detected by Western blotting, immunoprecipitation, or ELISA, etc. for the above purpose.

[0058] Furthermore, the antibody binding to the protein of the present invention can be utilized for treating the diseases that associates with the protein of the invention. If the antibodies are used for treating patients, human antibodies or humanized antibodies are preferable in terms of their low antigenicity. The human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of human ("Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez M.J. et al. (1997) *Nat. Genet.* 15: 146-156). The humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

[0059] The cDNA of the present invention encodes the amino acid sequence of a protein which is predicted to have the function(s) described below based on the homology search of the GenBank and SwissProt. Specifically, for instance, as shown in EXAMPLES, searching a known gene or protein that is homologous to the partial sequence of the full-length cDNA of the invention (5602 clone) and referring the function of the gene and of the protein encoded by the gene make it possible to predict the function of the protein encoded by the cDNA of the invention. In this way, each of 1437 clones out of the 5602 full-length cDNA clones of the invention was predicted to encode a protein that was classified into one or more of the following categories.

- Secretory or membrane protein (261 clones)
- Glycoprotein-associated protein (113 clones)
- Signal transduction-associated protein (148 clones)
- Transcription-associated protein (233 clones)
- Disease-associated protein (437 clones)
- Enzyme or metabolism-associated protein (301 clones)
- Cell division- or cell proliferation-associated protein (74 clones)
- Cytoskeleton-associated protein (92 clones)
- RNA synthesis-associated protein (280 clones)
- Nuclear protein (352 clones)
- Protein synthesis- or transport-associated protein (112 clones)
- Cellular defense-associated protein (23 clones)
- Development- or growth-associated protein (23 clones)

[0060] It is also possible to predict the protein function by looking into the amino acid sequence for the motifs such

as the signal sequence, transmembrane region, nuclear translocation signal, glycosylation signal, phosphorylation site, Zinc finger motif, and SH3 domain. The programs, PSORT (Nakai K., and Kanehisa M. (1992) *Genomics* 14: 897-911), SOSUI (Hirokawa T. et al. (1998) *Bioinformatics* 14: 378-379) (Mitsui Information Developing Inc.), and MEMSAT (Jones D.T., Taylor W.R., and Thornton J.M. (1994) *Biochemistry* 33: 3038-3049) can be used to predict the existence of the signal sequence or transmembrane region. Alternatively, a partial amino acid sequence of the protein is fused with another protein such as GFP, the fusion protein is transfected into cultured cells, and the localization is analyzed to predict the function of the original protein.

[0061] Based on the determined nucleotide sequences of the full-length cDNAs obtained in the present invention, it is possible to predict more detailed functions of the proteins encoded by the cDNA clones, for example, by searching the databases such as GenBank, Swiss-Prot and UniGene for homologies of the cDNAs; or by searching the amino acid sequences deduced from the full-length cDNAs for signal sequences by using software programs such as PSORT, for transmembrane regions by using software programs such as SOSUI or for motifs by using software programs such as Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) and PROSITE (<http://www.expasy.ch/prosite/>). As a matter of course, the functions are often predictable by using partial sequence information (preferably 300 nucleotides or more) instead of the full-length nucleotide sequences. However, the result of the prediction by using partial nucleotide sequence does not always agree with the result obtained by using full-length nucleotide sequence, and thus, it is needless to say that the prediction of function is preferably performed based on the full-length nucleotide sequences. GenBank, Swiss-Prot and UniGene databases were searched for homologies of the full-length nucleotide sequences of the 4997 clones (see Example 18). The amino acid sequences deduced from the full-length nucleotide sequences were searched for functional domains by PSORT, SOSUI and Pfam. Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based on these results obtained.

The following 798 clones were categorized into secretory and/or membrane proteins.

HEMBA1000356,	HEMBA1000518,	HEMBA1000531,	HEMBA1000637,	HEMBA1000719,	HEMBA1000817,
HEMBA1000822,	HEMBA1000852,	HEMBA1000870,	HEMBA1000991,	HEMBA1001052,	HEMBA1001071,
HEMBA1001085,	HEMBA1001286,	HEMBA1001351,	HEMBA1001407,	HEMBA1001446,	HEMBA1001515,
HEMBA1001557,	HEMBA1001569,	HEMBA1001661,	HEMBA1001734,	HEMBA1001746,	HEMBA1001866,
HEMBA1002125,	HEMBA1002150,	HEMBA1002166,	HEMBA1002417,	HEMBA1002462,	HEMBA1002475,
HEMBA1002477,	HEMBA1002486,	HEMBA1002609,	HEMBA1002659,	HEMBA1002661,	HEMBA1002780,
HEMBA1002818,	HEMBA1002876,	HEMBA1002921,	HEMBA1003071,	HEMBA1003077,	HEMBA1003079,
HEMBA1003086,	HEMBA1003096,	HEMBA1003281,	HEMBA1003286,	HEMBA1003538,	HEMBA1003711,
HEMBA1003742,	HEMBA1003803,	HEMBA1004055,	HEMBA1004143,	HEMBA1004146,	HEMBA1004207,
HEMBA1004341,	HEMBA1004461,	HEMBA1004577,	HEMBA1004637,	HEMBA1004752,	HEMBA1004756,
HEMBA1004850,	HEMBA1004889,	HEMBA1004923,	HEMBA1004930,	HEMBA1005029,	HEMBA1005035,
HEMBA1005050,	HEMBA1005552,	HEMBA1005576,	HEMBA1005581,	HEMBA1005588,	HEMBA1005616,
HEMBA1005699,	HEMBA1005991,	HEMBA1006036,	HEMBA1006038,	HEMBA1006067,	HEMBA1006173,
HEMBA1006198,	HEMBA1006293,	HEMBA1006310,	HEMBA1006492,	HEMBA1006502,	HEMBA1006583,
HEMBA1006659,	HEMBA1006758,	HEMBA1006789,	HEMBA1006921,	HEMBA1006926,	HEMBA1006976,
HEMBA1007203,	HEMBA1007301,	HEMBA1000037,	HEMBA1000050,	HEMBA1000054,	HEMBA1000175,
HEMBA1000317,	HEMBA1000556,	HEMBA1000593,	HEMBA1000631,	HEMBA1000763,	HEMBA1000827,
HEMBA1000915,	HEMBA1000975,	HEMBA1001112,	HEMBA1001151,	HEMBA1001177,	HEMBA1001302,
HEMBA1001348,	HEMBA1001564,	HEMBA1001630,	HEMBA1001871,	HEMBA1001872,	HEMBA1001925,
HEMBA1001962,	HEMBA1002042,	HEMBA1002044,	HEMBA1002142,	HEMBA1002190,	HEMBA1002193,
HEMBA1002247,	HEMBA1002383,	HEMBA1002387,	HEMBA1002550,	HEMBA1002600,	HEMBA1002692,
MAMMA1000045,	MAMMA1000129,	MAMMA1000133,	MAMMA1000277,	MAMMA1000278,	MAMMA1000410,
MAMMA1000416,	MAMMA1000472,	MAMMA1000672,	MAMMA1000684,	MAMMA1000714,	MAMMA1000734,
MAMMA1000778,	MAMMA1000798,	MAMMA1000842,	MAMMA1000859,	MAMMA1000897,	MAMMA1000956,
MAMMA1001008,	MAMMA1001030,	MAMMA1001041,	MAMMA1001073,	MAMMA1001080,	MAMMA1001139,
MAMMA1001154,	MAMMA1001322,	MAMMA1001388,	MAMMA1001411,	MAMMA1001487,	MAMMA1001751,
MAMMA1001754,	MAMMA1001771,	MAMMA1002009,	MAMMA1002427,	MAMMA1002428,	MAMMA1002461,
MAMMA1002524,	MAMMA1002573,	MAMMA1002598,	MAMMA1002655,	MAMMA1002684,	MAMMA1002769,
MAMMA1002844,	MAMMA1002881,	MAMMA1002890,	MAMMA1002938,	MAMMA1002947,	MAMMA1003035,
MAMMA1003089,	MAMMA1003146,	MAMMA1003150,	NT2RM1000035,	NT2RM1000037,	NT2RM1000062,
NT2RM1000080,	NT2RM1000092,	NT2RM1000131,	NT2RM1000199,	NT2RM1000257,	NT2RM1000260,
NT2RM1000355,	NT2RM1000430,	NT2RM1000563,	NT2RM1000648,	NT2RM1000742,	NT2RM1000770,
NT2RM1000800,	NT2RM1000811,	NT2RM1000833,	NT2RM1000857,	NT2RM1000867,	NT2RM1000882,
NT2RM1000905,	NT2RM1001008,				
NT2RM1001115,	NT2RM1001139,	NT2RM2000259,	NT2RM2000260,	NT2RM2000287,	NT2RM2000395,
NT2RM2000402,	NT2RM2000407,	NT2RM2000422,	NT2RM2000490,	NT2RM2000522,	NT2RM2000566,

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PLACE1009113, PLACE1011858, PLACE4000014, THYRO1000684, Y79AA1002139, Y79AA1002229

[0076] Although it is unclear whether or not 261 clones out of clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using their full-length sequences.

5 HEMBA1000030, HEMBA1000307, HEMBA1000333, HEMBA1000488, HEMBA1000523, HEMBA1001197,
HEMBA1001302, HEMBA1001455, HEMBA1001675, HEMBA1001714, HEMBA1001744, HEMBA1001967,
HEMBA1002151, HEMBA1002215, HEMBA1002458, HEMBA1002777, HEMBA1003098, HEMBA1003199,
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Y79AA1001923, Y79AA1002083, Y79AA1002307, Y79AA1002311, Y79AA1002487,

[0077] In some cases, the predicted functions based on the partial sequences are different from those based on the full-length sequences. The reason is that a protein does not always belong solely to a single category of the above-described functional categories, and therefore, a protein may belong to two or more of the predicted functional categories. Besides, additional functions can be found for the clones classified into these functional categories by further analyses.

[0078] Since the protein encoded by clones of the invention contains full-length amino acid sequence, it is possible to analyze its biological activity, and its effect on cellular conditions such as cell proliferation and differentiation by expressing the protein as a recombinant protein using an appropriate expression system, injecting the recombinant into the cell, or raising a specific antibody against the protein.

[0079] If the protein is a secretory protein, membrane protein, or protein associated with glycoprotein, signal trans-

duction, or transcription, its biological activity can be analyzed by the methods in "Gene Transcription" (Hames B.D., and Higgins S.J. edit, (1993)), "Glycobiology" (Fukuda M., and Kobata A. edit, (1993)), "Growth Factors" (McKay I., and Leigh I. edit, (1993)), "Extracellular Matrix" (Haralson M.A., and Hassell J.R. edit, (1995)), "Transcription Factors" (Latchman D.S. edit, (1993)), "Signal Transduction" (Milligans G. edit, (1992)), "Protein Phosphorylation" (Hardies G. D. edit, (1993)), and "Ion Channels" (Ashley R.H. edit, (1995)) featured in "The Practical Approach Series" (IRL PRESS), or "Signal Transduction Protocols" (Kendall D.A., and Hill S.J. edit, (1995)), "Glycoprotein Analysis in Biomedicine" (Hounsell E.F. edit, (1993)), featured in "Method in Molecular Biology" (Humana Press).

[0080] As to a protein associated with a disease, it is possible to perform a functional analysis as described above, but also possible to analyze correlation between the expression or the activity of the protein and a certain disease by using a specific antibody that is obtained by using expressed protein. Alternatively, it is possible to utilize the database Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is a database of human genes and diseases, to analyze the protein.

New information is constantly being deposited in the OMIM database. Therefore, it is possible for one skilled in the art to find a new relationship between a particular disease and a gene of the present invention in the most up-to-date database.

[0081] Also, as for a secretory protein, membrane protein, signal transduction-associated protein, glycoprotein-associated protein, or transcription-associated protein, etc., search of the OMIM with the following keywords resulted in the finding that the proteins are associated with many diseases (the result of the OMIM search for secrete and membrane proteins is shown below). Also, association between proteins associated to signal transduction or transcription and diseases is reported in "Transcription Factor Research-1999" (Fujii, Tamura, Kageyama, and Satake edit, (1999) Jikken-Igaku Zoukan, Vol.17, No.3), and "Gene Medicine" ((1999) Vol.3, No.2). For example, in tumors, many proteins have been shown to play a role, including secretory proteins, membrane proteins, and proteins associated with signal transduction, glycoprotein, and transcription, and also proteins associated with metabolism, cytoskeleton, and cell cycle, as described in "Tumor Biology" (Matsubara S. (1992) Syoukabou Life Science series). Thus, besides the proteins associated with diseases, many proteins described above are also potentially associated with diseases, and thus useful as a target in the medicinal industry.

[0082] The result of the OMIM search for secretory and membrane proteins is shown below, in which the keywords,

- (1) secretion protein,
- (2) membrane protein,
- (3) channel, and
- (4) extracellular matrix were used.

[0083] Shown in the search result are only the accession numbers in the OMIM. Using the number, data showing the relationship between a disease and a gene or protein can be seen. The OMIM data has been renewed everyday.

1) Secretion protein

268 entries found, searching for "secretion protein"

104760, 176860, 160900, 107400, 118910, 139320, 603850, 147572, 176880, 600946, 603215, 157147, 600174, 151675, 170280, 179512, 179513, 138120, 179509, 246700, 179510, 600626, 179511, 600998, 109270, 601489, 154545, 179490, 185860, 603216, 122559, 601746, 147290, 602672, 146770, 603062, 179508, 131230, 601591, 602421, 139250, 167805, 167770, 600041, 600564, 118825, 601146, 300090, 600753, 601652, 600759, 600768, 602434, 182590, 603166, 308230, 602534, 603489, 107470, 150390, 104610, 173120, 158106, 143890, 306900, 308700, 134797, 137350, 227500, 176300, 107730, 600760, 138079, 120180, 120160, 120150, 124092, 138160, 101000, 227600, 600509, 601199, 142410, 104311, 193400, 201910, 107300, 122560, 272800, 217000, 590050, 147670, 133170, 176730, 300300, 134370, 274600, 120140, 162151, 158070, 152790, 120120, 106100, 300200, 192340, 190160, 138040, 147470, 147620, 173350, 147380, 152200, 152760, 157145, 153450, 264080, 113811, 600937, 600840, 188545, 202110, 600514, 186590, 603372, 136435, 137241, 252800, 214500, 207750, 138850, 139191, 142640, 138130, 189907, 603692, 600633, 603355, 107270, 600377, 147892, 232200, 600281, 232800, 602358, 137035, 601771, 601769, 253200, 601933, 118444, 600270, 120700, 600945, 603732, 147660, 600761, 172400, 600823, 600877, 130080, 171060, 107740, 307800, 602843, 130660, 152780, 124020, 601124, 601340, 601604, 601610, 171050, 312060, 232700, 300159, 142703, 600734, 125255, 168450, 123812, 188540, 147940, 188450, 600839, 182452, 188400, 182280, 176760, 263200, 600264, 188826, 252650, 601185, 162641, 137216, 601398, 601538, 118888, 118445, 601745, 190180, 601922, 182098, 602008, 147440, 602384, 600031, 109160, 602663, 151670, 602682, 602730, 602779, 146880, 603061, 142704, 603140, 106150, 600732, 153620, 603318, 139392, 600042, 102200, 603493, 182100, 264300, 603795, 184600

2) Membrane protein

1017 entries found, searching for "membrane protein"

EP 1 074 617 A2

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3) Channel (member of membrane protein)

272 entries found, searching for "channel"

176266, 600724, 170500, 182390, 123825, 114208, 114205, 601784, 114206, 600937, 114204, 603415, 600053, 114209, 114207, 600760, 118425, 601011, 192500, 176261, 600761, 176260, 600359, 600228, 600877, 602235, 300008, 182389, 182391, 601328, 601534, 600504, 602323, 601958, 602780, 602781, 601327, 601012, 600734, 603208, 182392, 603220, 603219, 603888, 600054, 602232, 601745, 603537, 602604, 603796, 302910, 602866, 601013, 602905, 602906, 600163, 152427, 180901, 600702, 600308, 602754, 107776, 602024, 314555, 601949, 600235, 602023, 176263, 600681, 176265, 193245, 603305, 176258, 602983, 601219, 601141, 176267, 602343, 602726, 138253, 176262, 600003, 600397, 602872, 138249, 600843, 600935, 600580, 600845, 602158, 602106, 176264, 300110, 176257, 602717, 603493, 176268, 600932, 602727, 138254, 603652, 300138, 602420, 600570, 600150, 603583, 602345, 603749, 601142, 176256, 600846, 138252, 602982, 603787, 602836, 603788, 602566, 603651, 602421, 100690, 107777, 100725, 100710, 600509, 603061, 154275, 304040, 154276, 180902, 121014, 602368, 139311, 601383, 108745, 601313, 601042, 600131, 186360, 600109, 600229, 600170, 603319, 601485, 118503, 180903, 602076, 124030, 601059, 601212, 601218, 147450, 600855, 600919, 601154, 601157, 171060, 600968, 182139, 131230, 121015, 600421, 113730, 249210, 310500, 600637, 125950, 118800, 156490, 602974, 104610, 121011, 602522, 118504, 300041, 160900, 601382, 602103, 600465, 602014, 600442, 601109, 602481, 277900, 254210, 138247, 164920, 170280, 171050, 128100, 173910, 600884, 123885, 602887, 600232, 180297, 137192, 600304, 138251, 603053, 300103, 603152, 603199, 118511, 118508, 138079, 600983, 182307, 603324, 305990, 603418, 114080, 232200, 600046, 600040, 602403, 603750, 603785, 104210, 600019, 600300, 182860, 603852, 603853, 603855, 516060

4) Extracellular matrix

167 entries found, searching for "extracellular matrix"

603479, 602201, 601418, 601548, 154870, 115437, 602285, 602262, 602261, 134797, 600754, 120361, 116935, 602263, 603320, 601807, 603321, 185250, 185261, 253700, 128239, 120324, 193300, 276901, 308700, 600514, 600261, 602109, 120140, 120150, 147557, 193400, 600536, 188826, 120180, 118661, 120320, 152200, 135821, 112260, 230740, 602090, 155760, 192975, 190182, 602108, 601463, 186745, 600900, 600985, 600758, 602369, 179590, 601211, 600065, 602178, 600262, 182888, 182889, 151510, 182120, 150325, 190181, 150370, 186355, 193065, 165070, 154705, 147559, 146650, 146640, 153619, 175100, 187380, 231050, 188060, 135820, 156790, 130660, 301870, 128240, 600076, 600119, 193210, 600215, 600245, 121010, 150240, 600309, 600491, 222600, 120328, 600564, 600596, 600616, 600700, 600742, 120325, 138297, 600930, 156225, 601028, 601050, 601105, 253800, 601284, 601313, 120280, 310200, 601492, 120250, 601587, 601636, 601652, 601692, 601728, 120220, 601915, 602048, 155120, 310300, 120210, 120165, 120120, 118940, 116930, 602264, 116806, 602366, 120470, 602415, 602428, 602453, 602505, 602574, 603005, 603196, 603221, 603319, 107269, 216550, 103320, 603489, 603551, 603767, 603799, 603842

[0084] There are several methods for analyzing the expression levels of genes associated with diseases. Differences in gene expression levels between diseased and normal tissues are studied by the analytical methods, for example, Northern hybridization and differential display. Other examples include a method with high-density cDNA filter, a method with DNA microarray and methods with PCR amplification (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Naba (eds.), Shunjunsya). The varying levels of gene expression between diseased tissues and normal tissues can be studied by any of these analytical methods. When explicit difference in the expression level is observed for a gene, it can be concluded that the gene is closely associated with a disease or disorder. Instead of diseased tissues, cultured cells can be used

for the assessment. Similarly, when gene expression is explicitly different between normal cells and cells reproducing disease-associated specific features, it can be concluded that the gene is closely associated with a disease or disorder. When the expression levels of genes are evidently varied during major cellular events (such as differentiation and apoptosis), the genes are involved in the cellular events and accordingly are candidates for disease- and/or disorder-associated genes. Further, genes exhibiting tissue-specific expression are genes playing important parts in the tissue functions and, therefore, can be candidates for genes associated with diseases and/or disorders affecting the tissues.

[0085] For example, non-enzymic protein glycation reaction is believed to be a cause for a variety of chronic diabetic complications. Accordingly, genes of which expression levels are elevated or decreased in a glycated protein-dependent manner in the endothelial cells, are associated with diabetic complications caused by glycated proteins (Diabetes 1996, 45 (Suppl. 3), S67-S72; Diabetes, 1997, 46 (Suppl. 2), S19-S25).

The onset of rheumatoid arthritis is thought to be involved in the proliferation of synovial cells covering inner surfaces of joint cavity and in inflammatory reaction resulted from the action of cytokines produced by leukocytes infiltrating into the joint synovial tissues (Rheumatism Information Center, <http://www.rheuma-net.or.jp/>). Recent studies have also revealed that tissue necrosis factor (TNF)- α participates in the onset (Current opinion in immunology 1999, 11, 657-662). When the expression of a gene exhibits responsiveness to the action of TNF on synovial cells, the gene is considered to be involved in rheumatoid arthritis. Many genes acting at the downstream of TNF- α and IL-1 β among inflammation-associated cytokines have been previously identified. The respective stimulations are transduced through independent pathways of signaling cascade. There exists another signaling cascade for both stimulations, wherein NF- κ B is a common transducing molecule shared by the two stimulations (J. Leukoc. Biol., 1994, 56(5): 542-547). It has also been revealed that many inflammation-associated genes, including IL-2, IL-6 and G-CSF, are varied in the expression levels thereof in response to the signal through the common pathway (Trend Genet. 1999, 15(6): 229-235). It is assumed that genes of which expression levels are varied in response to the stimulation of TNF- α or IL-1 β also participate in inflammation.

[0086] Ultraviolet radiation damage has been recognized as a risk factor for skin cancers, etc. (United States Environmental Protection Agency: Ozone Depletion Home Page, <http://www.epa.gov/ozone/>). Genes of which expression levels are varied in skin epidermal cells exposed to ultraviolet rays are considered to be associated with ultraviolet radiation damage of skin. In addition, genes associated with neural differentiation can be candidates for genes responsible for neurological diseases as well as candidates for genes usable for treating the diseases.

[0087] Clones exhibiting differences in the expression levels thereof can be selected by using gene expression analysis. The selection comprises, for example; analyzing cDNA clones by using high-density cDNA filter; and statistically treating the multiple signal values (signal values of radioisotope in the labeled probes or values obtained by measuring fluorescence intensities emitted from the fluorescent labels) for the respective clones by two-sample t-test, where the signal values are determined by multiple experiments of hybridization. The clones of interest are selectable based on the statistically significant differences in the signal distribution at $p < 0.05$. However, selectable clones with significant difference in the expression levels thereof may be changed depending on the partial modification of statistical treatment. For example, the clones may be selected by conducting statistical treatment with two-sample t-test at $p < 0.01$; or genes exhibiting more explicit differences in the expression levels thereof can be selected by performing statistical treatment with a pre-determined cut-off value for the significant signal difference. An alternative method is that the expression levels are simply compared with each other, and then, the clones of interest are selected based on the ratio of the expression levels thereof.

[0088] Clones that vary in their expression levels can also be selected by comparing the expression levels by PCR analysis, for example, by using the method of determining the band intensities representing the amounts of PCR products with ethidium bromide staining; the method of determining the values of radioisotope signals or fluorescence intensities of the PCR products when radiolabeled or fluorescent dye-labeled primers, respectively, are used in PCR amplification; or the method of determining the values of radioisotope signals or fluorescence intensities of the probes hybridized to the PCR products when radiolabeled or fluorescent dye-labeled probes, respectively, are used in the hybridization. If the expression level ratios obtained in multiple PCR experiments are constantly at least 2-fold, such a clone can be judged to vary in its expression level. When the ratios are several-fold or not less than 10-fold, the clone can be selected as a gene exhibiting the explicit difference in its expression level.

[0089] A survey of genes of which expression levels are varied specifically to the glycated protein in the endothelial cells has revealed genes with elevated expression levels, HEMBA1003958, HEMBA1004850, MAMMA1001256, MAMMA1002132, PLACE2000411 and PLACE3000119. On the other hand, a gene of which expression level is decreased specifically to the glycated protein is MAMMA1001783. These clones are genes associated with diabetes.

[0090] A survey of genes of which expression levels are varied in response to TNF- α (Tumor Necrosis Factor-alpha) in the primary cell culture of synovial tissue has revealed the following clones with elevated expression levels in the presence of TNF- α :

HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000046, HEMBA1000076, HEMBA1000111, HEMBA1000168, HEMBA1000185, HEMBA1000201, HEMBA1000231, HEMBA1000243, HEMBA1000280,

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	HEMBA1000282,	HEMBA1000304,	HEMBA1000307,	HEMBA1000327,	HEMBA1000356,	HEMBA1000376,
	HEMBA1000387,	HEMBA1000390,	HEMBA1000418,	HEMBA1000460,	HEMBA1000491,	HEMBA1000501,
	HEMBA1000518,	HEMBA1000519,	HEMBA1000520,	HEMBA1000531,	HEMBA1000534,	HEMBA1000542,
	HEMBA1000545,	HEMBA1000591,	HEMBA1000592,	HEMBA1000594,	HEMBA1000636,	HEMBA1000655,
5	HEMBA1000657,	HEMBA1000673,	HEMBA1000682,	HEMBA1000686,	HEMBA1000722,	HEMBA1000726,
	HEMBA1000827,	HEMBA1000870,	HEMBA1000918,	HEMBA1000971,	HEMBA1000974,	HEMBA1000986,
	HEMBA1001019,	HEMBA1001043,	HEMBA1001051,	HEMBA1001059,	HEMBA1001060,	HEMBA1001071,
	HEMBA1001080,	HEMBA1001109,	HEMBA1001140,	HEMBA1001172,	HEMBA1001196,	HEMBA1001213,
	HEMBA1001226,	HEMBA1001281,	HEMBA1001299,	HEMBA1001302,	HEMBA1001303,	HEMBA1001323,
10	HEMBA1001326,	HEMBA1001327,	HEMBA1001330,	HEMBA1001351,	HEMBA1001407,	HEMBA1001411,
	HEMBA1001446,	HEMBA1001454,	HEMBA1001569,	HEMBA1001647,	HEMBA1001714,	HEMBA1001800,
	HEMBA1001804,	HEMBA1001809,	HEMBA1001888,	HEMBA1001912,	HEMBA1001921,	HEMBA1001967,
	HEMBA1002084,	HEMBA1002161,	HEMBA1002166,	HEMBA1002241,	HEMBA1002337,	HEMBA1002363,
	HEMBA1002389,	HEMBA1002458,	HEMBA1002460,	HEMBA1002469,	HEMBA1002538,	HEMBA1002542,
15	HEMBA1002547,	HEMBA1002609,	HEMBA1002624,			
	HEMBA1002659,	HEMBA1002750,	HEMBA1002770,	HEMBA1002779,	HEMBA1002810,	HEMBA1002816,
	HEMBA1002818,	HEMBA1002850,	HEMBA1002863,	HEMBA1003021,	HEMBA1003033,	HEMBA1003078,
	HEMBA1003166,	HEMBA1003202,	HEMBA1003204,	HEMBA1003229,	HEMBA1003235,	HEMBA1003276,
	HEMBA1003286,	HEMBA1003296,	HEMBA1003370,	HEMBA1003376,	HEMBA1003403,	HEMBA1003418,
20	HEMBA1003433,	HEMBA1003447,	HEMBA1003560,	HEMBA1003569,	HEMBA1003571,	HEMBA1003591,
	HEMBA1003597,	HEMBA1003598,	HEMBA1003621,	HEMBA1003656,	HEMBA1003662,	HEMBA1003680,
	HEMBA1003715,	HEMBA1003725,	HEMBA1003729,	HEMBA1003733,	HEMBA1003742,	HEMBA1003773,
	HEMBA1003783,	HEMBA1003950,	HEMBA1004012,	HEMBA1004015,	HEMBA1004048,	HEMBA1004074,
	HEMBA1004086,	HEMBA1004111,	HEMBA1004131,	HEMBA1004202,	HEMBA1004203,	HEMBA1004207,
25	HEMBA1004248,	HEMBA1004274,	HEMBA1004321,	HEMBA1004330,	HEMBA1004356,	HEMBA1004366,
	HEMBA1004405,	HEMBA1004408,	HEMBA1004429,	HEMBA1004499,	HEMBA1004507,	HEMBA1004509,
	HEMBA1004542,	HEMBA1004596,	HEMBA1004604,	HEMBA1004776,	HEMBA1004889,	HEMBA1004934,
	HEMBA1004978,	HEMBA1005019,	HEMBA1005047,	HEMBA1005206,	HEMBA1005219,	HEMBA1005274,
	HEMBA1005331,	HEMBA1005338,	HEMBA1005394,	HEMBA1005423,	HEMBA1005576,	HEMBA1005732,
30	HEMBA1005746,	HEMBA1006091,	HEMBA1006142,	HEMBA1006173,	HEMBA1006198,	HEMBA1006253,
	HEMBA1006268,	HEMBA1006309,	HEMBA1006377,	HEMBA1006474,	HEMBA1006486,	HEMBA1006492,
	HEMBA1006502,	HEMBA1006535,	HEMBA1006579,	HEMBA1006648,	HEMBA1006659,	HEMBA1006885,
	HEMBA1006929,	HEMBA1006941,	HEMBA1007078,	HEMBA1007080,	HEMBA1007121,	HEMBA1007194,
	HEMBA1007300,	HEMBA1007301,	HEMBA1007322,	HEMBA1000036,	HEMBA1000044,	HEMBA1000089,
35	HEMBA1000215,	HEMBA1000217,	HEMBA1000272,	HEMBA1000420,	HEMBA1000591,	HEMBA1000593,
	HEMBA1000631,	HEMBA1000835,	HEMBA1000887,	HEMBA1000908,	HEMBA1000975,	HEMBA1000985,
	HEMBA1001011,	HEMBA1001014,	HEMBA1001112,	HEMBA1001133,	HEMBA1001331,	HEMBA1001337,
	HEMBA1001366,	HEMBA1001367,	HEMBA1001384,	HEMBA1001394,	HEMBA1001429,	HEMBA1001463,
	HEMBA1001619,	HEMBA1001684,	HEMBA1001706,	HEMBA1001753,	HEMBA1001797,	HEMBA1001802,
40	HEMBA1001812,	HEMBA1001874,	HEMBA1001910,	HEMBA1001915,	HEMBA1001973,	HEMBA1001983,
	HEMBA1001990,	HEMBA1002190,	HEMBA1002193,	HEMBA1002249,	HEMBA1002329,	HEMBA1002342,
	HEMBA1002371,	HEMBA1002409,	HEMBA1002442,	HEMBA1002489,	HEMBA1002492,	HEMBA1002520,
	HEMBA1002534,	HEMBA1002596,	HEMBA1002664,	HEMBA1002692,	HEMBA1002697,	HEMBA1002705,
	MAMMA1000092,	MAMMA1000155,	MAMMA1000163,	MAMMA1000173,	MAMMA1000175,	MAMMA1000227,
45	MAMMA1000241,	MAMMA1000257,	MAMMA1000264,	MAMMA1000266,	MAMMA1000270,	MAMMA1000307,
	MAMMA1000410,	MAMMA1000413,	MAMMA1000416,	MAMMA1000421,	MAMMA1000472,	MAMMA1000501,
	MAMMA1000605,	MAMMA1000643,	MAMMA1000670,	MAMMA1000684,	MAMMA1000696,	MAMMA1000732,
	MAMMA1000752,	MAMMA1000802,	MAMMA1000824,	MAMMA1000905,	MAMMA1000921,	MAMMA1000931,
	MAMMA1000957,	MAMMA1000962,				
50	MAMMA1000998,	MAMMA1001008,	MAMMA1001050,	MAMMA1001074,	MAMMA1001078,	MAMMA1001292,
	MAMMA1001397,	MAMMA1001476,	MAMMA1001743,	MAMMA1001744,	MAMMA1001754,	MAMMA1001760,
	MAMMA1001785,	MAMMA1001858,	MAMMA1001908,	MAMMA1002236,	MAMMA1002267,	MAMMA1002292,
	MAMMA1002311,	MAMMA1002322,	MAMMA1002359,	MAMMA1002362,	MAMMA1002485,	MAMMA1002494,
	MAMMA1002597,	MAMMA1002598,	MAMMA1002665,	MAMMA1002671,	MAMMA1002684,	MAMMA1002748,
55	MAMMA1002775,	MAMMA1002830,	MAMMA1002858,	MAMMA1002868,	MAMMA1002886,	MAMMA1002887,
	MAMMA1002892,	MAMMA1002909,	MAMMA1002937,	MAMMA1002947,	MAMMA1002964,	MAMMA1002970,
	MAMMA1003013,	MAMMA1003150,	NT2RM1000039,	NT2RM1000062,	NT2RM1000080,	NT2RM1000086,
	NT2RM1000127,	NT2RM1000132,	NT2RM1000187,	NT2RM1000199,	NT2RM1000244,	NT2RM1000256,

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	NT2RM1000272,	NT2RM1000318,	NT2RM1000354,	NT2RM1000377,	NT2RM1000430,	NT2RM1000499,
	NT2RM1000539,	NT2RM1000553,	NT2RM1000563,	NT2RM1000699,	NT2RM1000742,	NT2RM1000826,
	NT2RM1000829,	NT2RM1000833,	NT2RM1000882,	NT2RM1000898,	NT2RM1000905,	NT2RM1001092,
	NT2RM2000013,	NT2RM2000032,	NT2RM2000042,	NT2RM2000101,	NT2RM2000124,	NT2RM2000192,
5	NT2RM2000259,	NT2RM2000260,	NT2RM2000363,	NT2RM2000368,	NT2RM2000402,	NT2RM2000452,
	NT2RM2000952,	NT2RM2001221,	NT2RM2002014,	NT2RM2002030,	NT2RM4000156,	NT2RM4000349,
	NT2RM4000395,	NT2RM4000457,	NT2RM4000511,	NT2RM4000514,	NT2RM4000698,	NT2RM4000764,
	NT2RM4001016,	NT2RM4001084,	NT2RM4001594,	NT2RM4001629,		
	NT2RM4001662,	NT2RM4001841,	NT2RM4002093,	NT2RM4002109,	NT2RM4002145,	NT2RM4002189,
10	NT2RM4002194,	NT2RM4002226,	NT2RP1000170,	NT2RP1000439,	NT2RP1000478,	NT2RP1000513,
	NT2RP1000701,	NT2RP1000856,	NT2RP1001361,	NT2RP2000097,	NT2RP2000239,	NT2RP2000288,
	NT2RP2000328,	NT2RP2000329,	NT2RP2000369,	NT2RP2000422,	NT2RP2000842,	NT2RP2000965,
	NT2RP2001245,	NT2RP2001440,	NT2RP2001560,	NT2RP2001634,	NT2RP2001663,	NT2RP2001677,
	NT2RP2001762,	NT2RP2002270,	NT2RP2002312,	NT2RP2002316,	NT2RP2002333,	NT2RP2002706,
15	NT2RP2002925,	NT2RP2002959,	NT2RP2002987,	NT2RP2003125,	NT2RP2003137,	NT2RP2003237,
	NT2RP2003272,	NT2RP2003596,	NT2RP2003604,	NT2RP2003643,	NT2RP2003968,	NT2RP2003976,
	NT2RP2004194,	NT2RP2004321,	NT2RP2005037,	NT2RP2005140,	NT2RP2005204,	NT2RP2005293,
	NT2RP2005457,	NT2RP2005555,	NT2RP2005600,	NT2RP2005701,	NT2RP2005719,	NT2RP2005722,
	NT2RP2005773,	NT2RP2005890,	NT2RP2006023,	NT2RP2006071,	NT2RP3000186,	NT2RP3000341,
20	NT2RP3000599,	NT2RP3000632,	NT2RP3000644,	NT2RP3000852,	NT2RP3000968,	NT2RP3001096,
	NT2RP3001109,	NT2RP3001126,	NT2RP3001147,	NT2RP3001449,	NT2RP3001529,	NT2RP3001753,
	NT2RP3001854,	NT2RP3001915,	NT2RP3001969,	NT2RP3002081,	NT2RP3002142,	NT2RP3002399,
	NT2RP3002590,	NT2RP3002603,	NT2RP3002810,	NT2RP3002876,	NT2RP3003311,	NT2RP3003330,
	NT2RP3003672,	NT2RP3004209,	NT2RP3004378,	NT2RP4000078,	NT2RP4000541,	NT2RP4000588,
25	NT2RP4001219,	NT2RP4001228,	NT2RP4001276,	NT2RP4001507,	NT2RP4002047,	NT2RP5003459,
	NT2RP5003492,	OVARC1000085,	OVARC1000087,	OVARC1000106,	OVARC1000151,	OVARC1000198,
	OVARC1000431,	OVARC1000440,	OVARC1000564,	OVARC1000605,	OVARC1000679,	OVARC1000883,
	OVARC1000912,	OVARC1000960,	OVARC1000971,	OVARC1001038,	OVARC1001055,	OVARC1001085,
	OVARC1001129,	OVARC1001167,	OVARC1001339,	OVARC1001425,	OVARC1001745,	OVARC1001762,
30	OVARC1001766,	OVARC1001942,	OVARC1002044,	OVARC1002138,	PLACE1000004,	PLACE1000005,
	PLACE1000420,	PLACE1000547,	PLACE1000562,	PLACE1000653,	PLACE1001168,	PLACE1001311,
	PLACE1001377,	PLACE1001920,	PLACE1001983,	PLACE1002066,	PLACE1002072,	PLACE1002140,
	PLACE1002171,	PLACE1002319,	PLACE1002474,	PLACE1002499,	PLACE1002532,	PLACE1002665,
	PLACE1003025,	PLACE1003145,	PLACE1003361,	PLACE1003605,	PLACE1003704,	PLACE1003783,
35	PLACE1003885,	PLACE1004405,	PLACE1004629,	PLACE1004686,	PLACE1004930,	PLACE1005066,
	PLACE1005077,	PLACE1005630,	PLACE1005876,	PLACE1006143,	PLACE1006325,	PLACE1006488,
	PLACE1006805,	PLACE1006829,	PLACE1007286,	PLACE1007858,	PLACE1008201,	PLACE1009045,
	PLACE1009113,	PLACE1009621,	PLACE1010106,	PLACE1010310,	PLACE1010622,	PLACE1010944,
	PLACE1010965,	PLACE1011185,	PLACE1011332,	PLACE1011635,	PLACE1011646,	PLACE1011725,
40	PLACE2000014,	PLACE2000264,	PLACE2000394,	PLACE2000419,	PLACE3000160,	PLACE3000220,
	PLACE3000254,	PLACE3000271,	PLACE3000339,	PLACE3000341,	PLACE3000350,	PLACE3000353,
	PLACE3000401,	PLACE4000300,	SKNMC1000091,	THYRO1000855,	THYRO1001559,	Y79AA1000065,
	Y79AA1000202,	Y79AA1000214,	Y79AA1000346,	Y79AA1000784,	Y79AA1000833,	Y79AA1000968,
	Y79AA1001555,	Y79AA1002220				
45	[0091] On the other hand, clones with decreased expression levels in the presence of TNF α are:					
	HEMBA1002150,	HEMBA1000240,	NT2RM2000469,	NT2RM2000984,	NT2RM2001688,	NT2RM4000290,
	NT2RM4000496,	NT2RM4000590,	NT2RM4001047,	NT2RM4001582,	NT2RM4001611,	NT2RM4001650,
	NT2RM4002075,	NT2RM4002128,	NT2RP1000174,	NT2RP1000243,	NT2RP1000581,	NT2RP1000688,
	NT2RP1000767,	NT2RP1000825,	NT2RP1001185,	NT2RP1001286,	NT2RP1001432,	NT2RP1001457,
50	NT2RP2000001,	NT2RP2000248,	NT2RP2000841,	NT2RP2001813,	NT2RP2002137,	NT2RP2002928,
	NT2RP2003517,	NT2RP2003559,	NT2RP2003564,	NT2RP2004933,	NT2RP2005038,	NT2RP2006365,
	NT2RP3000072,	NT2RP3000320,	NT2RP3000484,	NT2RP3000980,	NT2RP3001111,	NT2RP3001420,
	NT2RP3001495,	NT2RP3002056,	NT2RP3002057,	NT2RP3002545,	NT2RP3002713,	NT2RP3002799,
	NT2RP3002869,	NT2RP3002953,	NT2RP3002955,	NT2RP3003282,	NT2RP3003290,	NT2RP3003384,
55	NT2RP3003385,	NT2RP3003870,	NT2RP3004207,	NT2RP3004262,	NT2RP3004527,	NT2RP4000500,
	NT2RP4000524,	NT2RP4000787,	NT2RP4000927,	NT2RP4000955,	NT2RP4000989,	NT2RP4001442,
	NT2RP4001638,	NT2RP4001950,	NT2RP4002888,	NT2RP5003524,	OVARC1001270,	PLACE1000246,
	PLACE1002816,					

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[0092] These are rheumatoid arthritis-associated clones.

[0093] A survey of genes of which expression levels are varied in primary cultured skin fibroblast cells exposed to ultraviolet light has revealed the following clones with elevated expression levels by ultraviolet radiation:

HEMBA1000542, HEMBA1001808, HEMBA1002177, HEMBA1003314, MAMMA1001874, NT2RM2001100,
NT2RP2005732, NT2RP3000592, NT2RP4000657, OVARC 1000004, OVARC1001092, OVARC1001342,
PLACE1002816, NT2RM4001002, NT2RM4001813, NT2RM4002266, NT2RP2001174, NT2RP2001196,
NT2RP2005358, NT2RP3000690, NT2RP3001216, NT2RP3003464, PLACE1006382, THYRO1000070,
THYRO1001100, Y79AA1000342

[0094] On the other hand, the expression levels of the following clones were decreased by ultraviolet radiation:

HEMBA1000005, HEMBA1000150, HEMBA1000156, HEMBA1000158, HEMBA1000168, HEMBA1000231,
HEMBA1000304, HEMBA1000307, HEMBA1000333, HEMBA1000366, HEMBA1000369, HEMBA1000390,
HEMBA1000396, HEMBA1000418, HEMBA1000434, HEMBA1000464, HEMBA1000469, HEMBA1000490,
HEMBA1000504, HEMBA1000505, HEMBA1000557, HEMBA1000657, HEMBA1000673, HEMBA1000682,
HEMBA1000686, HEMBA1000727, HEMBA1000752, HEMBA1000851, HEMBA1000852, HEMBA1000870,
HEMBA1000872, HEMBA1001085, HEMBA1001121, HEMBA1001133, HEMBA1001235, HEMBA1001265,
HEMBA1001281, HEMBA1001289, HEMBA1001299, HEMBA1001303, HEMBA1001310, HEMBA1001323,
HEMBA1001595, HEMBA1001620, HEMBA1001640, HEMBA1001678, HEMBA1001712, HEMBA1001835,
HEMBA1001950, HEMBA1001987, HEMBA1002253, HEMBA1002321, HEMBA1002341, HEMBA1002419,
HEMBA1002679, HEMBA1002728, HEMBA1002818, HEMBA1002935, HEMBA1002999, HEMBA1003034,
HEMBA1003071, HEMBA1003098, HEMBA1003142, HEMBA1003175, HEMBA1003202, HEMBA1003212,
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35	PLACE1003361,	PLACE1003366,	PLACE1003369,	PLACE1003420,	PLACE1003454,	PLACE1003553,
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40	PLACE1004646,	PLACE1004722,	PLACE1004793,	PLACE1004804,	PLACE1004838,	PLACE1004868,
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	PLACE1006335,	PLACE1006360,	PLACE1006385,	PLACE1006412,	PLACE1006414,	PLACE1006445,
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	PLACE1007243,	PLACE1007454,	PLACE1007547,	PLACE1007598,	PLACE1007618,	PLACE1007645,
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50	PLACE1008273,	PLACE1008275,	PLACE1008331,	PLACE1008356,	PLACE1008368,	PLACE1008402,
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5	PLACE3000155,	PLACE3000169,	PLACE3000208,	PLACE3000230,	PLACE3000322,	PLACE3000331,
	PLACE3000352,	PLACE3000401,	PLACE3000413,	PLACE3000425,	PLACE3000477,	PLACE4000009,
	PLACE4000049,	PLACE4000089,	PLACE4000100,	PLACE4000247,	PLACE4000250,	PLACE4000252,
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10	THYRO1000173,	THYRO1000190,	THYRO1000197,	THYRO1000221,	THYRO1000253,	THYRO1000270,
	THYRO1000279,	THYRO1000327,	THYRO1000394,	THYRO1000438,	THYRO1000558,	THYRO1000569,
	THYRO1000585,	THYRO1000596,	THYRO1000625,	THYRO1000637,	THYRO1000676,	THYRO1000734,
	THYRO1000777,	THYRO1000783,	THYRO1000805,	THYRO1000843,	THYRO1000934,	THYRO1001033,
	THYRO1001347,	THYRO1001405,	THYRO1001411,	THYRO1001534,	THYRO1001573,	THYRO1001584,
15	THYRO1001602,	THYRO1001605,	THYRO1001772,	THYRO1001854,	VESEN1000122,	Y79AA1000037,
	Y79AA1000065,	Y79AA1000181,	Y79AA1000231,	Y79AA1000349,	Y79AA1000355,	Y79AA1000368,
	Y79AA1000538,	Y79AA1000782,	Y79AA1001023,	Y79AA1001145,	Y79AA1001391,	Y79AA1001541,
	Y79AA1001585,	Y79AA1001705,	Y79AA1001781,	Y79AA1001923,	Y79AA1001963,	Y79AA1002125,
	Y79AA1002229,	Y79AA1002407,	Y79AA1002487			
20	[0095] These clones are associated with ultraviolet radiation damage.					
	[0096] A survey of genes of which expression levels are varied in response to the stimulation for inducing cell differentiation (stimulation using retinoic acid (RA) or using RA/inhibitor (inhibitor for cell division)) in culture cells of neural strain, NT2, revealed the following clones with elevated expression levels in the presence of RA:					
	HEMBA1000005,	HEMBA1000042,	HEMBA1000046,	HEMBA1000076,	HEMBA1000111,	HEMBA1000141,
25	HEMBA1000150,	HEMBA1000185,	HEMBA1000282,	HEMBA1000304,	HEMBA1000307,	HEMBA1000338,
	HEMBA1000357,	HEMBA1000376,	HEMBA1000387,	HEMBA1000392,	HEMBA1000428,	HEMBA1000456,
	HEMBA1000459,	HEMBA1000469,	HEMBA1000504,	HEMBA1000508,	HEMBA1000519,	HEMBA1000540,
	HEMBA1000545,	HEMBA1000557,	HEMBA1000563,	HEMBA1000568,	HEMBA1000575,	HEMBA1000588,
	HEMBA1000592,	HEMBA1000604,	HEMBA1000622,	HEMBA1000655,	HEMBA1000673,	HEMBA1000682,
30	HEMBA1000726,	HEMBA1000727,	HEMBA1000749,	HEMBA1000769,	HEMBA1000774,	HEMBA1000791,
	HEMBA1000822,	HEMBA1000872,	HEMBA1000876,	HEMBA1000910,	HEMBA1000942,	HEMBA1000943,
	HEMBA1000960,	HEMBA1000972,	HEMBA1000974,	HEMBA1000991,	HEMBA1001008,	HEMBA1001020,
	HEMBA1001043,	HEMBA1001051,	HEMBA1001060,	HEMBA1001071,	HEMBA1001077,	HEMBA1001085,
	HEMBA1001094,	HEMBA1001109,	HEMBA1001121,	HEMBA1001122,	HEMBA1001140,	HEMBA1001172,
35	HEMBA1001226,	HEMBA1001235,	HEMBA1001265,	HEMBA1001281,	HEMBA1001294,	HEMBA1001299,
	HEMBA1001319,	HEMBA1001323,	HEMBA1001330,	HEMBA1001351,	HEMBA1001361,	HEMBA1001377,
	HEMBA1001388,	HEMBA1001391,	HEMBA1001398,	HEMBA1001432,	HEMBA1001435,	HEMBA1001442,
	HEMBA1001454,	HEMBA1001455,	HEMBA1001497,	HEMBA1001517,	HEMBA1001569,	HEMBA1001570,
	HEMBA1001581,	HEMBA1001585,	HEMBA1001620,	HEMBA1001711,	HEMBA1001718,	HEMBA1001723,
40	HEMBA1001761,	HEMBA1001815,	HEMBA1001819,	HEMBA1001861,	HEMBA1001864,	HEMBA1001869,
	HEMBA1001888,	HEMBA1001915,	HEMBA1001918,	HEMBA1001940,	HEMBA1001964,	HEMBA1001967,
	HEMBA1001979,	HEMBA1001987,	HEMBA1001991,	HEMBA1002008,	HEMBA1002022,	HEMBA1002039,
	HEMBA1002049,	HEMBA1002084,	HEMBA1002102,	HEMBA1002113,	HEMBA1002144,	HEMBA1002160,
	HEMBA1002162,	HEMBA1002185,	HEMBA1002212,	HEMBA1002226,	HEMBA1002229,	HEMBA1002267,
45	HEMBA1002270,	HEMBA1002337,	HEMBA1002381,	HEMBA1002458,	HEMBA1002477,	HEMBA1002508,
	HEMBA1002558,	HEMBA1002561,	HEMBA1002583,	HEMBA1002590,	HEMBA1002628,	HEMBA1002645,
	HEMBA1002661,	HEMBA1002678,	HEMBA1002712,	HEMBA1002728,	HEMBA1002780,	HEMBA1002850,
	HEMBA1002886,	HEMBA1002934,	HEMBA1002935,	HEMBA1002939,	HEMBA1002951,	HEMBA1002968,
	HEMBA1002970,	HEMBA1002973,	HEMBA1002999,	HEMBA1003021,	HEMBA1003033,	HEMBA1003034,
50	HEMBA1003064,	HEMBA1003067,	HEMBA1003078,	HEMBA1003086,	HEMBA1003096,	HEMBA1003129,
	HEMBA1003142,	HEMBA1003148,	HEMBA1003166,	HEMBA1003175,	HEMBA1003197,	HEMBA1003199,
	HEMBA1003202,	HEMBA1003204,	HEMBA1003212,	HEMBA1003235,	HEMBA1003250,	HEMBA1003273,
	HEMBA1003276,	HEMBA1003278,	HEMBA1003291,	HEMBA1003309,	HEMBA1003322,	HEMBA1003328,
	HEMBA1003348,	HEMBA1003369,	HEMBA1003376,	HEMBA1003384,	HEMBA1003395,	HEMBA1003463,
55	HEMBA1003480,	HEMBA1003531,	HEMBA1003548,	HEMBA1003591,	HEMBA1003595,	HEMBA1003597,
	HEMBA1003617,	HEMBA1003621,	HEMBA1003622,	HEMBA1003637,	HEMBA1003640,	HEMBA1003645,
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5	HEMBA1003838,	HEMBA1003879,	HEMBA1003885,	HEMBA1003893,	HEMBA1003908,	HEMBA1003937,
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10	HEMBA1004267,	HEMBA1004289,	HEMBA1004312,	HEMBA1004323,	HEMBA1004335,	HEMBA1004353,
	HEMBA1004354,	HEMBA1004356,	HEMBA1004366,	HEMBA1004396,	HEMBA1004405,	HEMBA1004429,
	HEMBA1004433,	HEMBA1004460,	HEMBA1004499,	HEMBA1004502,	HEMBA1004506,	HEMBA1004534,
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	HEMBA1005508,	HEMBA1005511,	HEMBA1005520,	HEMBA1005526,	HEMBA1005548,	HEMBA1005552,
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35	HEMBA1006973,	HEMBA1007017,	HEMBA1007052,	HEMBA1007080,	HEMBA1007085,	HEMBA1007113,
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35	NT2RM2001196,	NT2RM2001306,	NT2RM2001524,	NT2RM2001582,	NT2RM2001588,	NT2RM2001592,
	NT2RM2001605,	NT2RM2001632,	NT2RM2001637,	NT2RM2001648,	NT2RM2001668,	NT2RM2001671,
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40	NT2RM4000421,	NT2RM4000425,	NT2RM4000471,	NT2RM4000486,	NT2RM4000531,	NT2RM4000532,
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5	OVARC1000414,	OVARC1000442,	OVARC1000443,	OVARC1000486,	OVARC1000520,	OVARC1000526,
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15	PLACE3000121,	PLACE3000124,	PLACE3000155,	PLACE3000158,	PLACE3000207,	PLACE3000220,
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20	PLACE4000431,	PLACE4000445,	PLACE4000465,	PLACE4000487,	PLACE4000494,	PLACE4000522,
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	THYRO1000173,	THYRO1000190,	THYRO1000197,	THYRO1000221,	THYRO1000241,	THYRO1000327,
	THYRO1000381,	THYRO1000387,	THYRO1000394,	THYRO1000488,	THYRO1000585,	THYRO1000625,
25	THYRO1000637,	THYRO1000658,	THYRO1000666,	THYRO1000676,	THYRO1000684,	THYRO1000712,
	THYRO1000734,	THYRO1000793,	THYRO1000796,	THYRO1000805,	THYRO1000815,	THYRO1000865,
	THYRO1000916,	THYRO1000934,	THYRO1000974,	THYRO1000975,	THYRO1001031,	THYRO1001062,
	THYRO1001093,	THYRO1001133,	THYRO1001173,	THYRO1001177,	THYRO1001189,	THYRO1001204,
	THYRO1001213,	THYRO1001262,	THYRO1001290,	THYRO1001320,	THYRO1001322,	THYRO1001401,
30	THYRO1001406,	THYRO1001426,	THYRO1001480,	THYRO1001487,	THYRO1001537,	THYRO1001595,
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	Y79AA1001068,	Y79AA1001493,	Y79AA1001548,	Y79AA1001585,	Y79AA1001594,	Y79AA1001696,
35	Y79AA1001711,	Y79AA1002103,	Y79AA1002115,	Y79AA1002258,	Y79AA1002361,	Y79AA1002407,
	Y79AA1002472,	Y79AA1002482				
	[0097] On the other hand, clones of which expression levels decreased by RA are as follows:					
	HEMBA1000946,	HEMBA1003569,	HEMBA1005570,	HEMBA1000915,	NT2RM1000666,	NT2RM2000092,
	NT2RM2000594,	NT2RM2001256,	NT2RM4001754,	NT2RM4001905,	NT2RP2001675,	NT2RP2002047,
40	NT2RP2005491,	NT2RP3000980,	NT2RP3002081,	NT2RP3004594,	NT2RP4001950,	NT2RP4002408,
	OVARC1000431,	OVARC1001942,	OVARC1001943,	PLACE1003190,	PLACE1004868,	PLACE1005923,
	PLACE1007257,	PLACE1010624,	Y79AA1000346			
	[0098] Clones of which expression levels increase by RA/inhibitor are as follows:					
	HEMBA1000046,	HEMBA1000307,	HEMBA1000434,	HEMBA1000504,	HEMBA1000588,	HEMBA1000682,
45	HEMBA1000726,	HEMBA1000943,	HEMBA1001071,	HEMBA1001094,	HEMBA1001122,	HEMBA1001323,
	HEMBA1001361,	HEMBA1001455,	HEMBA1001709,	HEMBA1001746,	HEMBA1001869,	HEMBA1002084,
	HEMBA1002583,	HEMBA1002628,	HEMBA1002801,	HEMBA1002937,	HEMBA1003096,	HEMBA1003142,
	HEMBA1003229,	HEMBA1003276,	HEMBA1003309,	HEMBA1003463,	HEMBA1003597,	HEMBA1003617,
	HEMBA1003725,	HEMBA1003803,	HEMBA1003879,	HEMBA1003989,	HEMBA1004000,	HEMBA1004015,
50	HEMBA1004024,	HEMBA1004049,	HEMBA1004056,	HEMBA1004199,	HEMBA1004248,	HEMBA1004356,
	HEMBA1004554,	HEMBA1004666,	HEMBA1004725,	HEMBA1004770,	HEMBA1004803,	HEMBA1004923,
	HEMBA1004934,	HEMBA1004954,	HEMBA1005039,	HEMBA1005075,	HEMBA1005113,	HEMBA1005219,
	HEMBA1005232,	HEMBA1005251,	HEMBA1005304,	HEMBA1005367,	HEMBA1005372,	HEMBA1005403,
	HEMBA1005410,	HEMBA1005411,	HEMBA1005548,	HEMBA1005581,	HEMBA1005631,	HEMBA1005666,
55	HEMBA1005755,	HEMBA1005780,	HEMBA1006067,	HEMBA1006130,	HEMBA1006364,	HEMBA1006485,
	HEMBA1006559,	HEMBA1006579,	HEMBA1006754,	HEMBA1000059,	HEMBA1000575,	HEMBA1000709,
	HEMBA1000822,	HEMBA1000848,	HEMBA1000852,	HEMBA1000913,	HEMBA1000985,	HEMBA1001117,
	HEMBA1001210,	HEMBA1001317,	HEMBA1001394,	HEMBA1001443,	HEMBA1001668,	HEMBA1001695,

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	HEMBB1002049,	HEMBB1002254,	HEMBB1002266,	HEMBB1002371,	HEMBB1002502,	HEMBB1002614,
	HEMBB1002617,	HEMBB1002692,	HEMBB1002697,	MAMMA1000241,	MAMMA1000424,	MAMMA1000616,
	MAMMA1000731,	MAMMA1000824,	MAMMA1000908,	MAMMA1000956,	MAMMA1001038,	MAMMA1001091,
	MAMMA1001243,	MAMMA1001815,	MAMMA1001820,	MAMMA1002267,	MAMMA1002769,	MAMMA1002871,
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	NT2RM2001613,	NT2RM2001632,	NT2RM2001635,	NT2RM2001648,	NT2RM2001659,	NT2RM2001671,
	NT2RM2001695,	NT2RM2001760,	NT2RM2001782,	NT2RM2001839,	NT2RM2001879,	NT2RM2001983,
10	NT2RM4000104,	NT2RM4000290,	NT2RM4000425,	NT2RM4000433,	NT2RM4000471,	NT2RM4000531,
	NT2RM4000852,	NT2RM4001047,	NT2RM4001347,	NT2RM4001454,	NT2RM4001557,	NT2RM4001566,
	NT2RM4001582,	NT2RM4001938,	NT2RM4001953,	NT2RM4002018,	NT2RM4002409,	NT2RM4002558,
	NT2RM4002594,	NT2RP1000259,	NT2RP1000418,	NT2RP1000574,	NT2RP1000629,	NT2RP1000782,
	NT2RP1000856,	NT2RP1000943,	NT2RP1000988,	NT2RP1001013,	NT2RP1001173,	NT2RP1001546,
15	NT2RP2000091,	NT2RP2000208,	NT2RP2000274,	NT2RP2000329,	NT2RP2000369,	NT2RP2000634,
	NT2RP2000842,	NT2RP2000943,	NT2RP2000987,	NT2RP2001094,	NT2RP2001277,	NT2RP2001290,
	NT2RP2001366,	NT2RP2001423,	NT2RP2001436,	NT2RP2001467,	NT2RP2001506,	NT2RP2001601,
	NT2RP2001663,	NT2RP2001926,	NT2RP2001985,	NT2RP2002032,	NT2RP2002041,	NT2RP2002046,
	NT2RP2002078,	NT2RP2002124,	NT2RP2002185,	NT2RP2002193,	NT2RP2002312,	NT2RP2002316,
20	NT2RP2002426,	NT2RP2002457,	NT2RP2002475,	NT2RP2002520,	NT2RP2002595,	NT2RP2002643,
	NT2RP2002672,	NT2RP2002701,	NT2RP2002710,	NT2RP2002727,	NT2RP2003099,	NT2RP2003121,
	NT2RP2003137,	NT2RP2003158,	NT2RP2003206,	NT2RP2003230,	NT2RP2003272,	NT2RP2003280,
	NT2RP2003347,	NT2RP2003393,	NT2RP2003401,	NT2RP2003445,	NT2RP2003456,	NT2RP2003511,
	NT2RP2003517,	NT2RP2003543,	NT2RP2003596,	NT2RP2003706,	NT2RP2003871,	NT2RP2004681,
25	NT2RP2004743,	NT2RP2004775,	NT2RP2004933,	NT2RP2004967,	NT2RP2005003,	NT2RP2005270,
	NT2RP2005289,	NT2RP2005344,	NT2RP2005453,	NT2RP2005555,	NT2RP2005767,	NT2RP2005853,
	NT2RP2006043,	NT2RP2006393,	NT2RP2006436,	NT2RP2006441,	NT2RP2006467,	NT2RP2006534,
	NT2RP2006565,	NT2RP3000348,	NT2RP3000359,	NT2RP3000366,	NT2RP3000403,	NT2RP3000418,
	NT2RP3000441,	NT2RP3000561,	NT2RP3000759,	NT2RP3000826,	NT2RP3001007,	NT2RP3001096,
30	NT2RP3001126,	NT2RP3001355,	NT2RP3001396,	NT2RP3001449,	NT2RP3001490,	NT2RP3001679,
	NT2RP3001727,	NT2RP3001752,	NT2RP3001777,	NT2RP3001782,	NT2RP3001799,	NT2RP3001854,
	NT2RP3001989,	NT2RP3002142,	NT2RP3002248,	NT2RP3002343,	NT2RP3002484,	NT2RP3002529,
	NT2RP3002549,	NT2RP3002628,	NT2RP3002687,	NT2RP3002688,	NT2RP3002810,	NT2RP3003032,
	NT2RP3003139,	NT2RP3003193,	NT2RP3003203,	NT2RP3003204,	NT2RP3003210,	NT2RP3003212,
35	NT2RP3003264,	NT2RP3003282,	NT2RP3003500,	NT2RP3004041,	NT2RP3004215,	NT2RP4000147,
	NT2RP4000259,	NT2RP4000360,	NT2RP4000448,	NT2RP4000524,	NT2RP4000588,	NT2RP4000879,
	NT2RP4000907,	NT2RP4000989,	NT2RP4001079,	NT2RP4001150,	NT2RP4001219,	NT2RP4001260,
	NT2RP4001274,	NT2RP4001353,	NT2RP4001547,	NT2RP4001677,	NT2RP4002052,	OVARC1000006,
	OVARC1000092,	OVARC1000321,	OVARC1000384,	OVARC1000408,	OVARC1000414,	OVARC1000520,
40	OVARC1000526,	OVARC1000588,	OVARC1000679,	OVARC1000682,	OVARC1000769,	OVARC1000850,
	OVARC1000862,	OVARC1000886,	OVARC1000984,	OVARC1001000,	OVARC1001004,	OVARC1001154,
	OVARC1001170,	OVARC1001173,	OVARC1001200,	OVARC1001268,	OVARC1001376,	OVARC1001419,
	OVARC1001425,	OVARC1001476,	OVARC1001480,	OVARC1001542,	OVARC1001873,	OVARC1001928,
	OVARC1001987,	OVARC1002066,	OVARC1002082,	OVARC1002112,	OVARC1002127,	
45	PLACE1000014,	PLACE1000048,	PLACE1000184,	PLACE1000185,	PLACE1000246,	PLACE1000292,
	PLACE1000332,	PLACE1000347,	PLACE1000564,	PLACE1000656,	PLACE1000712,	PLACE1001000,
	PLACE1001168,	PLACE1001185,	PLACE1001241,	PLACE1001294,	PLACE1001311,	PLACE1001395,
	PLACE1001570,	PLACE1001608,	PLACE1001610,	PLACE1001716,	PLACE1001746,	PLACE1001817,
	PLACE1001821,	PLACE1001844,	PLACE1001897,	PLACE1002066,	PLACE1002119,	PLACE1002157,
50	PLACE1002205,	PLACE1002256,	PLACE1002259,	PLACE1002399,	PLACE1002438,	PLACE1002474,
	PLACE1002477,	PLACE1002500,	PLACE1002514,	PLACE1002578,	PLACE1002815,	PLACE1002851,
	PLACE1002968,	PLACE1003108,	PLACE1003174,	PLACE1003200,	PLACE1003238,	PLACE1003256,
	PLACE1003334,	PLACE1003342,	PLACE1003516,	PLACE1003521,	PLACE1003537,	PLACE1003592,
	PLACE1003596,	PLACE1003723,	PLACE1003760,	PLACE1003771,	PLACE1003783,	PLACE1003795,
55	PLACE1003892,	PLACE1003968,	PLACE1004103,	PLACE1004256,	PLACE1004405,	PLACE1004460,
	PLACE1004506,	PLACE1004629,	PLACE1004674,	PLACE1004813,	PLACE1004979,	PLACE1005066,
	PLACE1005101,	PLACE1005102,	PLACE1005128,	PLACE1005181,	PLACE1005287,	PLACE1005305,
	PLACE1005327,	PLACE1005477,	PLACE1005595,	PLACE1005603,	PLACE1005666,	PLACE1005804,

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PLACE1005884, PLACE1005934, PLACE1006076, PLACE1006119, PLACE1006159, PLACE1006164,
 PLACE1006170, PLACE1006382, PLACE1006492, PLACE1006629, PLACE1006704, PLACE1006731,
 PLACE1006760, PLACE1006779, PLACE1006795, PLACE1006805, PLACE1006962, PLACE1007045,
 PLACE1007111, PLACE1007282, PLACE1007386, PLACE1007416, PLACE1007484, PLACE1007544,
 5 PLACE1007645, PLACE1007743, PLACE1007746, PLACE1007807, PLACE1007858, PLACE1008002,
 PLACE1008181, PLACE1008273, PLACE1008368, PLACE1008405, PLACE1008532, PLACE1008568,
 PLACE1008625, PLACE1008696, PLACE1008867, PLACE1009027, PLACE1009039, PLACE1009045,
 PLACE1009110, PLACE1009298, PLACE1009328, PLACE1009581, PLACE1009621, PLACE1009622,
 PLACE1009637, PLACE1009925, PLACE1009935, PLACE1010089, PLACE1010106, PLACE1010152,
 10 PLACE1010274, PLACE1010491, PLACE1010629, PLACE1010630, PLACE1010714, PLACE1010739,
 PLACE1010891, PLACE1010896, PLACE1010925, PLACE1010965, PLACE1011026, PLACE1011046,
 PLACE1011214, PLACE1011399, PLACE1011433, PLACE1011492, PLACE1011641, PLACE1011649,
 PLACE1011719, PLACE1011762, PLACE1011858, PLACE1011923, PLACE2000014, PLACE2000039,
 PLACE2000216, PLACE2000302, PLACE2000317, PLACE2000342, PLACE2000347, PLACE2000379,
 15 PLACE3000121, PLACE3000124, PLACE3000160, PLACE3000242, PLACE3000271, PLACE3000353,
 PLACE3000362, PLACE3000365, PLACE3000400, PLACE3000401, PLACE4000034, PLACE4000089,
 PLACE4000522, PLACE4000558,
 SKNMC1000050, THYRO1000040, THYRO1000197, THYRO1000241, THYRO1000327, THYRO1000394,
 THYRO1000488, THYRO1000501, THYRO1000585, THYRO1000596, THYRO1000625, THYRO1000805,
 20 THYRO1000934, THYRO1001133, THYRO1001134, THYRO1001173, THYRO1001213, THYRO1001262,
 THYRO1001290, THYRO1001721, Y79AA1000037, Y79AA1000800, Y79AA1000976, Y79AA1001078,
 Y79AA1001228, Y79AA1001299, Y79AA1001402, Y79AA1001585, Y79AA1001696, Y79AA1001711,
 Y79AA1001827, Y79AA1001875, Y79AA1002027, Y79AA1002211, Y79AA1002234, Y79AA1002258

[0099] On the other hand, clones of which expression levels decrease by RA/inhibitor are as follows:

25 HEMBA1000012, HEMBA1000501, HEMBA1000946, HEMBA1003220, HEMBA1003403, HEMBA1003569,
 HEMBA1003591, HEMBA1003926, HEMBA1004168, HEMBA1004507, HEMBA1005009, HEMBA1005296,
 HEMBA1005528, HEMBA1005570, HEMBA1006467, HEMBA1006486, HEMBA1006492, HEMBA1007322,
 HEMBB1000055, HEMBB1000244, HEMBB1001665, MAMMA1000684, MAMMA1001139, MAMMA1001743,
 NT2RM1000257, NT2RM1000318, NT2RM1000539, NT2RM1000666, NT2RM2000092, NT2RM2000192,
 30 NT2RM2000371, NT2RM2000594, NT2RM4000511, NT2RM4001140, NT2RM4001754, NT2RM4001905,
 NT2RM4001940, NT2RM4002593, NT2RP1000086, NT2RP1000439, NT2RP1001073, NT2RP2000098,
 NT2RP2000965, NT2RP2001397, NT2RP2002047, NT2RP2004226, NT2RP2004396, NT2RP2004655,
 NT2RP2005126, NT2RP2005464, NT2RP2005712, NT2RP2005859, NT2RP2005890, NT2RP3000980,
 NT2RP3001383, NT2RP3001621, NT2RP3002081, NT2RP3002181, NT2RP3002244, NT2RP3002590,
 35 NT2RP3003059, NT2RP3004258, NT2RP3004378, NT2RP3004527, NT2RP3004594, NT2RP4001760,
 NT2RP4001950, NT2RP4002047, NT2RP4002408, NT2RP5003459, OVARC1000004, OVARC1000035,
 OVARC1000431, OVARC1001051, OVARC1001129, OVARC1001176, OVARC1001261, OVARC1001342,
 OVARC1001942, OVARC1001943, PLACE1002171, PLACE1002465, PLACE1003190, PLACE1003375,
 PLACE1004128, PLACE1005026, PLACE1005876, PLACE1005923, PLACE1007257, PLACE1007375,
 40 PLACE1007507, PLACE1008941, PLACE1010624, PLACE1011090, PLACE1011219, THYRO1000270,
 Y79AA1000346, Y79AA1001541

[0100] These clones are also associated with neural differentiation and, therefore, are candidates for genes associated with neurological diseases.

[0101] For example, if the protein encoded by the cDNA of the present invention is a regulatory factor of cellular
 45 conditions such as growth and differentiation, it can be used for developing medicines as follows. The protein or antibody
 provided by the invention is injected into a certain kind of cells by microinjection. Then, using the cells, it is possible
 to screen low molecular weight compounds by measuring the change in the cellular conditions, or the activation or
 inhibition of a particular gene. The screening can be performed as follows. First, the protein is expressed and purified
 50 as recombinant. The purified protein is microinjected into cells such as various cell lines, or primary culture cells, and
 the cellular change such as growth and differentiation can be examined. Alternatively, the induction of genes whose
 expression is known to be associated with a particular change of cellular conditions may be detected by the amount
 of mRNA or protein. Or, the amount of intracellular molecules (low molecular weight compounds, etc.) that is changed
 by the function of the gene product (protein) which is known to be associated with a particular change of cellular
 conditions may be detected. The compounds to be screened (both low and high molecular compounds are acceptable)
 55 can be added to the culture media and assessed for their activity by measuring the change of the cellular conditions.
 Instead of microinjection, cell lines introduced with the gene obtained in the invention can be used for the screening.
 If the gene product is turn out to be associated with a particular change in the cellular conditions, the change of the
 product can be used as a measurement for screening. Once a compound is screened out which can activate or inhibit

the function of the protein of the invention, it can be applied for developing medicines.

[0102] If the protein encoded by the cDNA of the present invention is a secretory protein, membrane protein, or protein associated with signal transduction, glycoprotein, transcription, or diseases, it can be used in functional assays for developing medicines.

[0103] In case of a membrane protein, it is most likely to be a protein that functions as a receptor or ligand on the cell surface. Therefore, it is possible to reveal a new relationship between a ligand and receptor by screening the membrane protein of the invention based on the binding activity with the known ligand or receptor. Screening can be performed according to the known methods.

[0104] For example, a ligand against the protein of the invention can be screened in the following manner. Namely, a ligand that binds to a specific protein can be screened by a method comprising the steps of: (a) contacting a test sample with the protein of the invention or a partial peptide thereof, or cells expressing these, and (b) selecting a test sample that binds to said protein, said partial peptide, or said cells.

[0105] On the other hand, for example, screening using cells expressing the protein of the present invention that is a receptor protein can also be performed as follows. It is possible to screen receptors that is capable of binding to a specific protein by using procedures (a) attaching the sample cells to the protein of the invention or its partial peptide, and (b) selecting cells that can bind to the said protein or its partial peptide.

[0106] In a following screening as an example, first the protein of the invention is expressed, and the recombinant protein is purified. Next, the purified protein is labeled, binding assay is performed using a various cell lines or primary cultured cells, and cells that are expressing a receptor are selected (Growth and differentiation factors and their receptors, Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjo, Arai, Taniguchi, and Muramatsu edit, p203-236, Tokyo-Kagaku-Doujin). A protein of the invention can be labeled with RI such as ^{125}I , and enzyme (alkaline phosphatase etc.). Alternatively, a protein of the invention may be used without labeling and then detected by using a labeled antibody against the protein. The cells that are selected by the above screening methods, which express a receptor of the protein of the invention, can be used for the further screening of an agonists or antagonists of the said receptor.

[0107] Once the ligand binding to the protein of the invention, the receptor of the protein of the invention or the cells expressing the receptor are obtained by screening, it is possible to screen a compound that binds to the ligand and receptor. Also it is possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor, for example) by utilizing the binding activities.

[0108] When the protein of the invention is a receptor, the screening method comprises the steps of (a) contacting the protein of the invention or cells expressing the protein of the invention with the ligand, in the presence of a test sample, (b) detecting the binding activity between said protein or cells expressing said protein and the ligand, and (c) selecting a compound that reduces said binding activity when compared to the activity in the absence of the test sample. Furthermore, when the protein of the invention is a ligand, the screening method comprises the steps of (a) contacting the protein of the invention with its receptor or cells expressing the receptor in the presence of samples, (b) detecting the binding activity between the protein and its receptor or the cells expressing the receptor, and (c) selecting a compound that can potentially reduce the binding activity compared to the activity in the absence of the sample.

[0109] Samples to screen include cell extracts, expressed products from a gene library, synthesized low molecular compound, synthesized peptide, and natural compounds, for example, but are not construed to be listed here. A compound that is isolated by the above screening using a binding activity of the protein of the invention can also be used as a sample.

[0110] A compound isolated by the screening may be a candidate to be an agonist or an antagonist of the receptor of the protein. By utilizing an assay that monitors a change in the intracellular signaling such as phosphorylation which results from reduction of the binding between the protein and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the receptor. Also, the compound may be a candidate of a molecule that can inhibit the interaction between the protein and its associated proteins (including a receptor) in vivo. Such compounds can be used for developing drugs for precaution or cures of a disease with which the protein is associated.

[0111] Secretory proteins may regulate cellular conditions such as growth and differentiation. It is possible to find out a novel factor that regulates cellular conditions by adding the secretory protein of the invention to a certain kind of cell, and performing a screening by utilizing the cellular changes in growth or differentiation, or activation of a particular gene.

[0112] The screening can be performed, for example, as follows. First, the protein of the invention is expressed and purified in a recombinant form. Then, the purified protein is added to a various kind of cell lines or primary cultured cells, and the change in the cell growth and differentiation is monitored. The induction of a particular gene that is known to be involved in a certain cellular change is detected by the amounts of mRNA and protein. Alternatively, the amount of an intracellular molecule (low-molecular-weight compounds, etc.) that is changed by the function of a gene product (protein) that is known to function in a certain cellular change is used for the detection.

[0113] Once the screening reveals that the protein of the invention can regulate cellular conditions or the functions, it is possible to apply the protein as a pharmaceutical and diagnostic medicine for associated diseases by itself or by

altering a part of it into an appropriate composition.

[0114] As is above described for membrane proteins, the secretory protein provided by the invention may be used to explore a novel ligand-receptor interaction using a screening based on the binding activity to a known ligand or receptor. A similar method can be used to identify an agonist or antagonist. The resulting compounds obtained by the methods can be a candidate of a compound that can inhibit the interaction between the protein of the invention and an interacting molecule (including a receptor). The compounds may be able to use as a preventive, therapeutic, and diagnostic medicine for the diseases, in which the protein may play a certain role.

[0115] Proteins associated with signal transduction or transcription may be a factor that affects a certain protein or gene in response to intracellular/extracellular stimuli. It is possible to find out a novel factor that can affect a protein or gene by expressing the protein provided by the invention in a certain types of cells, and performing a screening utilizing the activation of a certain intracellular protein or gene.

[0116] The screening may be performed as follows. First, a transformed cell line expressing the protein is obtained. Then, the transformed cell line and the untransformed original cell line are compared for the changes in the expression of a certain gene by detecting the amount of its mRNA or protein. Alternatively, the amount of an intracellular molecule (low molecular weight compounds) that is changed by the function of a certain gene product (protein) may be used for the detection. Furthermore, the change of the expression of a certain gene can be detected by introducing a fusion gene that comprises a regulatory region of the gene and a marker gene (luciferase, beta-galactosidase, etc.) into a cell, expressing the protein provided by the invention into the cell, and estimating the activity of a marker gene product (protein).

[0117] If the protein or gene of the invention is associated with diseases, it is possible to screen a gene or compound that can regulate its expression and/or activity either directly or indirectly by utilizing the protein of the present invention.

[0118] For example, the protein of the invention is expressed and purified as a recombinant protein. Then, the protein or gene that interacts with the protein of the invention is purified, and screened based on the binding. Alternatively, the screening can be performed by adding with a compound of a candidate of the inhibitor added in advance and monitoring the change of binding activity. In another method, a transcription regulatory region locating in the 5'-upstream of the gene encoding the protein of the invention that is capable of regulating the expression of other genes is obtained, and fused with a marker gene. The fusion is introduced into a cell, and the cell is added with compounds to explore a regulatory factor of the expression of the said gene.

[0119] The compound obtained by the screening can be used for developing pharmaceutical and diagnostic medicines for the diseases with which the protein of the present invention is associated. Similarly, if the regulatory factor obtained in the screening is turn out to be a protein, compounds that can newly affect the expression or activity of the protein may be used as a medicine for the diseases with which the protein of the invention is associated.

[0120] If the protein of the invention has an enzymatic activity, regardless as to whether it is a secretory protein, membrane protein, or proteins associated with signal transduction, glycoprotein, transcription, or diseases, a screening may be performed by adding a compound to the protein of the invention and monitoring the change of the compound. The enzymatic activity may also be utilized to screen a compound that can inhibit the activity of the protein.

[0121] In a screening given as an example, the protein of the invention is expressed and the recombinant protein is purified. Then, compounds are contacted with the purified protein, and the amount of the compound and the reaction products is examined. Alternatively, compounds that are candidates of an inhibitor are pretreated, then a compound (substrate) that can react with the purified protein is added, and the amount of the substrate and the reaction products is examined.

[0122] The compounds obtained in the screening may be used as a medicine for diseases with which the protein of the invention is associated. Also they can be applied for tests that examine whether the protein of the invention functions normally *in vivo*.

[0123] Whether the secretory protein, membrane protein, signal transduction-associated protein, glycoprotein-associated protein, or transcription-associated protein of the present invention is a novel protein associated with diseases or not is determined in another method than described above, by obtaining a specific antibody against the protein of the invention, and examining the relationship between the expression or activity of the protein and a certain disease. In an alternative way, it may be analyzed referred to the methods in "Molecular Diagnosis of Genetic Diseases" (Elles R. edit, (1996) in the series of "Method in Molecular Biology" (Humana Press).

[0124] Proteins associated with diseases are targets of screening as mentioned, and thus are very useful in developing drugs which regulate their expression and activity. Also, the proteins are useful in the medicinal industry as a diagnostic marker of the associated disease or a target of gene therapy.

[0125] Compounds isolated as mentioned above can be administered patients as it is, or after formulated into a pharmaceutical composition according to the known methods. For example, a pharmaceutically acceptable carrier or vehicle, specifically sterilized water, saline, plant oil, emulsifier, or suspending agent can be mixed with the compounds appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial, intravenous, or subcutaneous injections. The dosage may vary depending on the weight

or age of a patient, or the method of administration, but those skilled in the art can choose an appropriate dosage properly. If the compound is encoded by DNA, the DNA can be cloned into a vector for gene therapy, and used for gene therapy. The dosage of the DNA and the method of its administration may vary depending on the weight or age of a patient, or the symptoms, but those skilled in the art can choose properly.

[0126] The present invention further relates to databases comprising at least a sequence of polynucleotide and/or protein, or a medium recorded in such databases, selected from the sequence data of the nucleotide and/or the amino acids indicated in Table 350 and Table 351.

The term "database" means a set of accumulated information as machine-searchable and readable information of nucleotide sequence. The databases of the present invention comprise at least one of the novel nucleotide sequences of polynucleotides provided by the present invention. The databases of the present invention can consist of only the sequence data of the novel polynucleotides provided by the present invention or can comprise other information on nucleotide sequences of known full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only the information on the nucleotide sequences but also the information on the gene functions revealed by the present invention. Additional information such as names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

[0127] The database of the present invention is useful for gaining complete gene sequence information from partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing the information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, the information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

[0128] The sequence information of the full-length cDNAs constituting the database of the present invention contains not only the information on the complete sequences but also extra information on expression frequency of the genes as well as homology of the genes to known genes and known proteins. Thus the extra information facilitates rapid functional analyses of partial gene fragments. Further, the information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from other species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

[0129] At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to an already-known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there exists no information corresponding to the partial sequence of interest in the known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using the partial sequence information as an initial clue. If the full-length of the gene is not available, the amino acid sequence of the protein encoded by the gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-length cDNAs corresponding to gene fragments, which cannot be revealed by using databases of known genes.

[0130] The present invention has provided 5602 novel full-length cDNA clones, and primers for synthesizing the cDNA. As has not yet proceeded the isolation of full-length cDNA within the human, the invention has great significance. The full-length cDNA clones contain the translation initiation site, and thus provide a useful information for analysis of protein functions.

[0131] The cDNA clones are assumed to encode proteins such as secretory proteins, membrane proteins, signal transduction-associated protein, glycoprotein-associated protein, or transcription-associated protein, etc., which have important functions in vivo, and also predicted to be associated with many diseases. The genes and proteins associated with diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0132] The invention is illustrated more specifically with reference to the following examples, but is not to be construed as being limited thereto.

EXAMPLE 1

Construction of a cDNA library by the oligo-capping method.

[0133] The NT-2 neuron progenitor cells (Stratagene), a teratocarcinoma cell line from human embryo testis, which can differentiate into neurons by the treatment with retinoic acid were used.

The NT-2 cells were cultured according to the manufacturer's instructions as follows.

- (1) NT-2 cells were cultured without induction by retinoic acid treatment (NT2RM1, NT2RM2, NT2RM4).
- (2) After cultured, NT-2 cells were induced by adding retinoic acid, and then were cultured for 48 hours (NT2RP1).

(3) After cultured, NT-2 cells were induced by adding retinoic acid, and then were cultured for 2 weeks (NT2RP2, NT2RP3, NT2RP4, NT2RP5).

[0134] Also, the human neuroblastoma cell line SK-N-MC (ATCC HTB-10) (SKNMC1), and human retinoblastoma cell line Y79 (ATCC HTB-18) (Y79AA1) were cultured according to the culture conditions described in the ATCC catalogue (<http://www.atcc.org/>). The cells were harvested separately, and mRNA was extracted from each cell by the method described in the literature (Molecular Cloning 2nd edition. (1989) Sambrook J., Fritsch, E.F., and Maniatis T., Cold Spring Harbor Laboratory Press). Furthermore, poly(A)+RNA was purified from the mRNA using oligo-dT cellulose.

[0135] Similarly, human placenta (PLACE1, PLACE2, PLACE3, PLACE4), human ovary cancer tissue (OVARC1), tissues from human embryo at 10 weeks, which is enriched with head (HEMBA1), or body (HEMBB1), human mammary gland (MAMMA1), human thyroid gland (THYRO1), and primary cultured cells of human blood vessel endothelium (VESEN1) were used to extract mRNA by the method described in the literature (Molecular Cloning 2nd edition. (1989) Sambrook J., Fritsch, E.F., and Maniatis T., Cold Spring Harbor Laboratory Press). Furthermore, poly(A)+RNA was purified from the mRNA using oligo-dT cellulose.

[0136] Each poly(A)+RNA was used to construct a cDNA library by the oligo-capping method (Maruyama M. and Sugano S. (1994) Gene, 138: 171-174). Using the Oligo-cap linker (SEQ ID NO: 10464) and the Oligo-dT primer (SEQ ID NO: 10465), bacterial alkaline phosphatase (BAP) treatment, tobacco acid phosphatase (TAP) treatment, RNA ligation, the first strand cDNA synthesis, and removal of RNA were performed as described in the reference (Suzuki and Kanno (1996) Protein Nucleic acid and Enzyme, 41: 197-201; Suzuki Y. et al. (1997) Gene, 200: 149-156). Next, 5'- and 3'-PCR primers (SEQ ID NO: 10466, and 10467, respectively) were used for performing PCR to convert the cDNA into double stranded cDNA, which was then digested with SfiI. Then, the DraIII-cleaved pUC19FL3 vector (Figure 1; for NT2RM1, and NT2RP1), or the DraIII-cleaved pME18SFL3 (Figure 1) (GenBank AB009864, expression vector; for NT2RM2, NT2RM4, NT2RP2, NT2RP3, NT2RP4, NT2RP5, SKNMC1, Y79AA1, PLACE1, PLACE2, PLACE3, PLACE4, OVARC1, HEMBA1, HEMBB1, MAMMA1, THYRO1, and VESEN1) was used for cloning the cDNA in a unidirectional manner, and cDNA libraries were obtained. The nucleotide sequence of the 5'- and 3'- ends of the cDNA clones was analyzed with a DNA sequencer (ABI PRISM 377, PE Biosystems) after sequencing reactions were performed with the DNA sequencing reagents (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit, or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems), according to the instructions. The data were compiled into a database.

[0137] The full-length-enriched cDNA libraries except those for NT2RM1 and NT2RP1 were constructed using eukaryotic expression vector pME18SFL3. The vector contains SR α promoter and SV40 small t intron in the upstream of the cloning site, and SV40 polyA added signal sequence site in the downstream. As the cloning site of pME18SFL3 has asymmetrical DraIII sites, and the ends of cDNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cDNA fragments can be inserted into the downstream of the SR α promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells. Thus, the clones can be analyzed very easily in terms of the proteins that are the gene products of the clones, or in terms of the biological activities of the proteins.

[0138] Herein, the cDNA libraries and the name of each clone are related as shown in Table 3. Therein, "xxxxxx" represents the clone number of six digits. Thus, the sequences are named by the library name, the clone number plus F- for the 5'-end, or R- for the 3'-end.

Table 3

	library: clone	5'-end sequence	3'-end sequence
5			
	NT2RM1 :		
10	NT2RM1xxxxxx	F-NT2RM1xxxxxx	
	NT2RP1 :		
	NT2RP1xxxxxx	F-NT2RP1xxxxxx	
	NT2RM2 :		
15	NT2RM2xxxxxx	F-NT2RM2xxxxxx	R-NT2RM2xxxxxx
	NT2RM4 :		
	NT2RM4xxxxxx	F-NT2RM4xxxxxx	R-NT2RM4xxxxxx
20			
25			
30			
35			
40			
45			
50			
55			

	NT2RP2:		
	NT2RP2xxxxxx	F-NT2RP2xxxxxx	R-NT2RP2xxxxxx
5	NT2RP3:		
	NT2RP3xxxxxx	F-NT2RP3xxxxxx	R-NT2RP3xxxxxx
	NT2RP4:		
10	NT2RP4xxxxxx	F-NT2RP4xxxxxx	R-NT2RP4xxxxxx
	NT2RP5:		
	NT2RP5xxxxxx	F-NT2RP5xxxxxx	R-NT2RP5xxxxxx
	SKNMC1:		
15	SKNMC1xxxxxx	F-SKNMC1xxxxxx	R-SKNMC1xxxxxx
	Y79AA1:		
	Y79AA1xxxxxx	F-Y79AA1xxxxxx	R-Y79AA1xxxxxx
	PLACE1:		
20	PLACE1xxxxxx	F-PLACE1xxxxxx	R-PLACE1xxxxxx
	PLACE2:		
	PLACE2xxxxxx	F-PLACE2xxxxxx	R-PLACE2xxxxxx
	PLACE3:		
25	PLACE3xxxxxx	F-PLACE3xxxxxx	R-PLACE3xxxxxx
	PLACE4:		
	PLACE4xxxxxx	F-PLACE4xxxxxx	R-PLACE4xxxxxx
	OVARC1:		
30	OVARC1xxxxxx	F-OVARC1xxxxxx	R-OVARC1xxxxxx
	HEMBA1:		
	HEMBA1xxxxxx	F-HEMBA1xxxxxx	R-HEMBA1xxxxxx
	HEMBA1:		
35	HEMBA1xxxxxx	F-HEMBA1xxxxxx	R-HEMBA1xxxxxx
	MAMMA1:		
	MAMMA1xxxxxx	F-MAMMA1xxxxxx	R-MAMMA1xxxxxx
	THYRO1:		
40	THYRO1xxxxxx	F-THYRO1xxxxxx	R-THYRO1xxxxxx
	VESEN1:		
45	VESEN1xxxxxx	F-VESEN1xxxxxx	R-VESEN1xxxxxx

EXAMPLE 2

Estimation of the fullness ratio at the 5'-ends of the clones contained in the cDNA libraries constructed by the oligo-capping method.

[0139] The fullness ratio at the 5'-end sequence of the 59,823 clones in the human cDNA libraries constructed by the oligo-capping method was determined as follows. Of all the clones whose 5'-end sequences were found in those of known human mRNA in the public database, a clone was judged to be "full-length", if it had a longer 5'-end sequence than that of the known human mRNA, or, even though the 5'-end sequence was shorter, if it contained the translation initiation codon. A clone which did not contain the translation initiation codon was judged to be "not-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and not-full-length clones)) at the 5'-end of the cDNA clones from each library was determined by comparing with the known human mRNA. As a result, the fullness

ratio of the 5'-ends was 63.5%. The result indicates that the fullness ratio at the 5'-end sequence was extremely high.

EXAMPLE 3

Assessment of the fullness ratio of the 5'-end of the cDNA by the ATGpr and the ESTiMateFL.

[0140] The ATGpr, developed by Salamov A.A., Nishikawa T., and Swindells M.B. in the Helix Research Institute, is a program for prediction of the translation initiation codon based on the characteristics of the sequences in the vicinity of the ATG codon. The results are shown with expectations (also described as ATGpr1 below) that an ATG is a true initiation codon (0.05-0.94) (can be described as ATGpr1). When the program was applied to the 5'-end sequences of the clones from the cDNA library that was obtained by the oligo-capping method and that had 65% fullness ratio, the sensitivity and specificity of estimation of a full-length clone (clone containing the N-terminal end of ORF) were improved to 82-83% by selecting only clones having the ATGpr1 score 0.6 or higher.

[0141] Furthermore, the program was used to assess the fullness of 18,959 clones in the human libraries obtained here, which have 5'-ends matched to a known human mRNA.

[0142] Briefly, the maximal ATGpr1 score of the clones was determined, and then their 5'-end sequence was compared with the known human mRNA to estimate whether the clone is full-length or not. The result is shown in Table 4.

[0143] Based on the knowledge that known mRNAs, in general, are highly expressed in the cell, similar estimation was performed with genes having a low number in the EST hit, which represent relatively low abundant mRNAs, and the result is shown in Table 5.

[0144] In the table, the number of full-length clones indicate that of clones containing the N-terminal end of ORF, and so does the number of not-full-length clones that of clones without the N-terminal end of ORF. The fullness ratio represents (the number of full-length clones)/(the number of full-length clones plus the number of not-full-length clones).

Table 4

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having a matched 5'-end with that of a known mRNA.			
maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
≥ 0.70	11,193	9,346	83.5%
≥ 0.50	13,369	10,549	78.9%
≥ 0.30	15,489	11,340	73.2%
≥ 0.15	17,394	11,811	67.9%
≥ 0.00	18,959	12,046	63.5%

Table 5

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of the clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having 5 EST hits or less among the clones having a matched 5'-end with that of a known mRNA.			
maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
≥ 0.70	2,801	1,934	69.0%
≥ 0.50	3,683	2,393	65.0%
≥ 0.30	4,683	2,707	57.8%
≥ 0.15	5,559	2,890	52.0%
≥ 0.00	6,113	3,013	49.8%

[0145] Next, the ESTiMateFL was used for the estimation. The ESTiMateFL, developed by Nishikawa and Ota in the Helix Research Institute, is a method for the selection of a clone with high fullness ratio by comparing with the 5'-end or 3'-end sequences of ESTs in the public database.

[0146] By the method, a cDNA clone is judged to be most likely not to be full-length if there exist any ESTs which

have longer 5'-end or 3'-end sequences than the clone. The method is systematized for high throughput analysis. A clone is judged to be full-length if the clone has a longer 5'-end sequence than ESTs in the public database. Even if a clone has a shorter 5'-end, the clone is judged to be full-length if the difference in length is within 50 bases, and otherwise judged not to be full-length, for convenience.

[0147] In case of the clones whose 5'-end sequence is matching with the known mRNA, 80% of the clones judged to be full-length by comparing with ESTs was also judged to be full-length by comparing with the known mRNA. Also, 80% of the clones judged to be not full-length by comparing with ESTs was also judged to be not full-length by comparing with the known mRNA.

[0148] The precision of the estimation by comparing with ESTs is improved with increasing number of ESTs to be compared. However, in case that a limited number of ESTs are available, the reliability becomes low. Thus, the method is effective in excluding clones with high probability of being not-full-length, from the cDNA clones that is synthesized by the oligo-capping method and that have the 5'-end sequences with about 60 % fullness ratio. In particular, the ESTiMateFL is efficiently used to estimate the fullness ratio at the 3'-end sequence of cDNA of a human unknown mRNA which has a significant number of EST deposits in the public database.

[0149] The 18,959 clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence matched with a known human mRNA, were estimated by using the ATGpr and ESTiMateFL. Briefly, the 5'-end sequence of the respective clone was analyzed to obtain the maximal ATGpr1 score, and compared with the ORF of the known human mRNA that matches with it to determine whether the clone is full-length or not. Then, the 5'-end sequence of the respective clone was analyzed by the ESTiMateFL to judge whether the clone is full-length or not. Specifically, the 5'-end sequences of the 18,959 clones were compared with those of ESTs by the ESTiMateFL and the clones other than those that are not full-length were selected. Then, the selected clones were used to analyze the relationship between the ATGpr and the fullness ratio. The result was summarized in Table 6. Also, among the selected, the clones in which the number of the EST hit is not more than 5 were selected and analyzed. The result was summarized in Table 7, which represents the result of the analysis of mRNA with relatively low abundance.

[0150] Therein, the number of being full-length, the number of being not full-length, and the fullness ratio indicate the number of the clones that contain the N-terminus of the ORF, the number of the clones that do not contain the N-terminus of the ORF, and (the number of being full-length)/(the number of being full-length plus (the number of being not full-length)), respectively.

Table 6

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequence in the clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence matched with a known human mRNA, and also other than those being not full-length according to the comparison with ESTs.			
maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
≥ 0.70	9,068	8,349	92.1%
≥ 0.50	10,345	9,318	90.1%
≥ 0.30	11,425	9,964	87.2%
≥ 0.15	12,254	10,335	84.3%
≥ 0.00	12,785	10,484	82.0%

Table 7

Maximal ATGpr1 score and fullness ratio of the 5'-end sequence of the clones, which were isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to a known human mRNA, in which the number of the EST hit is not more than 5.			
maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
≥ 0.70	1,959	1,510	77.1%
≥ 0.50	2,469	1,821	73.8%
≥ 0.30	2,975	2,046	68.8%
≥ 0.15	3,368	2,164	64.3%

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Table 7 (continued)

Maximal ATGpr1 score and fullness ratio of the 5'-end sequence of the clones, which were isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to a known human mRNA, in which the number of the EST hit is not more than 5.			
maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
≥ 0.00	3,661	2,226	60.8%

[0151] The 19,226 clones, isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to that of a known human mRNA were estimated by the ATGpr2, and the correlation between the score and the fullness ratio was estimated. Specifically, the maximal ATGpr2 score of the clones identical to a known human mRNA was determined, and then their fullness ratio was estimated by comparing the 5'-ends with ORF of known human mRNA. The result was shown in Table 8.

Table 8

Maximal ATGpr2 score and fullness ratio of the 5'-end sequence of the clones, which are isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to a known human mRNA.			
maximal ATGpr2 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
≥ 0.30	10,748	8,031	74.7%
≥ 0.15	16,383	11,226	68.5%
≥ 0.00	19,226	12,285	63.9%

[0152] According to the above results, it was found that, in case of using clones isolated from human cDNA libraries constructed by the oligo-capping method, the fullness ratio of the clones that have low score in the ATGpr can be improved by estimating their 5'-end sequence using the combination of the ATGpr and the ESTiMateFL. Therefore, the method was applied to select a cDNA clone with high fullness ratio.

EXAMPLE 4

Clustering of the 5'-end and 3'-end sequences of cDNA clones.

[0153] The 5'-end and 3'-end sequences of cDNA clones were obtained, and clustered separately. The single pass data of the nucleotide sequence of the 5'-end and 3'-end was subject to the BLAST search between the sequence data of all the clones synthesized in example 1, and the clones considered to be originating from the same gene were put together into a group. If the 5'-end of a clone contains the consensus sequence of 300 bases or more with identity 95% or more, or the 3'-end contains the consensus sequence of 200 bases or more and having identity 90% or more, the clones were put in the same group.

[0154] The groups of the 5'-end sequence and the 3'-end sequence were further clustered so as that the groups from the same clone can be in the same group (cluster).

EXAMPLE 5

Characterization of the cloned sequence.

[0155] The data of the 5'-end sequence of the cloned sequence was characterized by the following way:

- (1) examining whether it is identical to those of mRNA from human and other species (including authorized sequences) and human EST by the BLAST homology search of the GenBank,
- (2) examining whether it has longer 5'-end than those of human mRNA and human EST,
- (3) determining the scores in the ATGpr1 and ATGpr2 programs of all the initiation codons in the 5'-end sequence, and

(4) determining the number of the human EST clone(s) that is judged to be identical by the BLAST homology search of the GenBank.

[0156] The data of the 3'-end sequence of the cloned sequence was characterized by the above (1) and (4).

[0157] These characterized data were used for the final selection of the clones.

EXAMPLE 6

Identity to the human mRNA and human EST, and comparison of the length of the 5'-end.

[0158] The 5'-end and 3'-end sequences of the cloned sequence was judged to be identical to those of mRNA from human or other species when the sequence to compare has the length of 200 bases or longer, and the obtained homology is 94% or more. The 5'-end and 3'-end sequences of the cloned sequence was judged to be identical to those of human EST when the sequence to compare has the length of 200 bases or longer, and the obtained homology is 90% or more.

[0159] The sequence of the clone was judged to be full-length in comparison with human mRNA when the sequence has longer 5'-end, or it contains the translation initiation site. The sequence of the clone was judged to be full-length in comparison with human EST in the database when the sequence has longer 5'-end, or while it has shorter end, the difference in length between the two sequences is 50 bases or less. The other clones were judged to be not full-length.

EXAMPLE 7

Prediction of the fullness ratio by the ATGpr.

[0160] The score in the ATGpr1 is the expectation to be full-length based on calculations, and the higher score reflects the higher probability to be full-length as shown in Example 3. The maximal ATGpr1 score and the maximal ATGpr2 score represent the score obtained with all the initiation codons contained in the 5'-end sequence of the cloned sequence, and were used for the characterization.

EXAMPLE 8

Prediction of the novelty using the number of the identical ESTs by the homology search.

[0161] For both the 5'-end and 3'-end sequences of the clones, the number of the identical ESTs was determined by the homology search on the GenBank. Human ESTs were judged to be identical when the EST has a sequence of 200 nucleotides or more with 90% or more matching with the 5'-end sequence. The number of the identical ESTs were used for characterization and as an index of novelty. The clone having not identical sequence at the 5'-end and 3'-end sequences to those of mRNA as well as those of ESTs is a gene encoding a novel protein. Similarly, a clone having either the 5'-end or the 3'-end sequences, which has low number of the identical ESTs, is judged to be a gene encoding a novel protein.

EXAMPLE 9

Characterization of clusters.

[0162] The clusters of the groups of the 5'-end and 3'-end sequences were characterized according to the following criteria.

(1) Whether it is identical to the mRNA sequences from human or other species (including authorized sequences), or human ESTs by the BLAST search of the GenBank.

A cluster containing at least one sequence of all the 5'-end and 3'-end sequences, which is identical to one of the mRNA sequences, was regarded to be the same cluster of the mRNA sequence.

(2) Whether it has longer 5'-end than human mRNA sequence and human ESTs.

When all the 5'-end sequences contained in a cluster are judged to be not full-length compared with the mRNA sequences and human ESTs, the cluster was regarded as being not full-length.

(3) The scores in the ATGpr1 and ATGpr2 using all the initiation codons contained in the 5'-end sequences.

The maximal ATGpr1 score among those of all the 5'-end sequences in a cluster was determined as the ATGpr1 score of the cluster. The ATGpr2 score of the cluster was also determined in the same way.

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(4) The number of the identical human ESTs determined by the BLAST search of the GenBank.

[0163] The maximum number was determined in the numbers of ESTs identical to each of 5'-end sequences contained in a cluster. The number of the ESTs identical to the 5'-end sequences in the cluster was defined as the maximum number. The number of the ESTs identical to the 3'-end sequences in a cluster was determined in the same way.

EXAMPLE 10

Methods for selection of the clusters by the characteristics.

[0164] Data obtained by the characterization described above was used to discard the clusters that are identical to any mRNA sequence from human and other species (including authorized sequences), or those clusters that are not full-length. From the rest of the clusters, the clusters that fulfill any of the following conditions were selected.

(a) A cluster in which the number of the identical ESTs for the 5'-end sequence is 20 or less, and the ATGpr1 score exceeds 0.3.

(b) A cluster having the ATGpr1 score not more than 0.3, in which the number of the identical ESTs for both the 5'-end sequence and the 3'-end sequence is 5 or less, and multiple clones are contained.

(c) A cluster having the ATGpr1 score not more than 0.3, in which the number of the identical ESTs for the 5'-end sequence is 0, and the number of the identical ESTs for the 3'-end sequence is not less than 1.

(d) A cluster having the ATGpr1 score not more than 0.3, in which the number of the identical ESTs for the 5'-end sequence is not less than 1 and not more than 5, and the number of the identical ESTs for the 3'-end sequence is 0.

[0165] The clusters selected by (a) contain at least one clone that is novel and having high fullness ratio. The clusters selected by (b), (c), and (d) contain at least one clone that is novel and having low fullness ratio, but is still full-length.

EXAMPLE 11

Methods for selection of clones from clusters.

[0166] In the clusters comprising a single clone, the clone was selected.

[0167] In the clusters comprising multiple clones, in which multiple clones have the ATGpr1 score higher than 0.3, a clone with the highest score was selected.

[0168] In the clusters comprising multiple clones, in which multiple clones have the ATGpr1 score not more than 0.3, a clone with the highest ATGpr2 score was selected, if the score was higher than 0.3.

[0169] In the clusters comprising multiple clones, in which the clones have the scores not more than 0.3 in both the ATGpr1 and the ATGpr2, a clone with the highest scores in both the ATGpr1 and ATGpr2 was selected.

[0170] In the clusters comprising multiple clones, in which the above selection by the ATGpr score was not applicable, selected was a clone having longer 5'-end by assembling the 5'-end sequence, 3'-end sequence, and human ESTs. For assembling, the Sequencher™ (Hitachi Soft Engineering) was used. When even the selection by assembling failed, all the clones were judged to be full-length.

[0171] As a result, 3690 clones were the clones that have the maximal ATGpr1 score higher than 0.3. On the other hand, 477 clones were the clones that have the maximal ATGpr1 score not more than 0.3, and the maximal ATGpr2 score higher than 0.3. The number of the clones having the highest scores in both the ATGpr1 and ATGpr2, while the scores were not more than 0.3, were 97. The number of the clones which were not selected by the ATGpr scores, but were selected by assembling the 5'-end sequence, 3'-end sequence, and human ESTs, were 117. The clones that have the score in both the ATGpr1 and ATGpr2 not more than 0.3, but were selected because the cluster comprises a single clone, were 1166. In the clones, at least either of the 5'-end or 3'-end sequence was not identical to any of human ESTs. Some clones were selected because the cluster comprises a single clone, or by assembling, in which there is no ATG codon (9 clones: HEMBA1001960, HEMBA106569, HEMBB1001454, NT2PR2002839, NT2RP2005325, NT2RP2006323, PLACE1004506, PLACE1005526, and THYRO1001177). The sequences that do not contain the ATG codon were considered to be corresponding to the 5'-UTR. Although the clones do not have the scores in the ATGpr1 and ATGpr2, the clones were yet judged to be full-length according to the fullness ratio, as shown in Table 4, 5, 6, 7, and 8. The above clones that were finally judged to be full-length were classified into 11 groups according to the following criteria.

Group (1): 1516 clones

Among the 3690 clones having the maximal ATGpr1 score higher than 0.3, the following 1516 clones were having

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high fullness ratio and a novel clone, in which at least either of the 5'-end or 3'-end sequence, or both of them were not identical to any of human ESTs.

	HEMBA1000046,	HEMBA1000050,	HEMBA1000129,	HEMBA1000150,	HEMBA1000158,	HEMBA1000193
	HEMBA1000201,	HEMBA1000216,	HEMBA1000227,	HEMBA1000288,	HEMBA1000290,	HEMBA1000303
5	HEMBA1000304,	HEMBA1000369,	HEMBA1000392,	HEMBA1000396,	HEMBA1000488,	HEMBA1000505
	HEMBA1000508,	HEMBA1000534,	HEMBA1000542,	HEMBA1000594,	HEMBA1000637,	HEMBA1000657
	HEMBA1000752,	HEMBA1000867,	HEMBA1000869,	HEMBA1000872,	HEMBA1000910,	HEMBA1000918
	HEMBA1000919,	HEMBA1000942,	HEMBA1000968,	HEMBA1000975,	HEMBA1000986,	HEMBA1001022
	HEMBA1001043,	HEMBA1001052,	HEMBA1001080,	HEMBA1001085,	HEMBA1001109,	HEMBA1001140
10	HEMBA1001174,	HEMBA1001235,	HEMBA1001286,	HEMBA1001302,	HEMBA1001398,	HEMBA1001407
	HEMBA1001415,	HEMBA1001446,	HEMBA1001476,	HEMBA1001497,	HEMBA1001510,	HEMBA1001533
	HEMBA1001570,	HEMBA1001581,	HEMBA1001635,	HEMBA1001640,	HEMBA1001647,	HEMBA1001661
	HEMBA1001731,	HEMBA1001744,	HEMBA1001746,	HEMBA1001800,	HEMBA1001815,	HEMBA1001822
	HEMBA1001866,	HEMBA1001896,	HEMBA1001910,	HEMBA1001987,		
15	HEMBA1002018,	HEMBA1002035,	HEMBA1002049,	HEMBA1002092,	HEMBA1002119,	HEMBA1002125
	HEMBA1002161,	HEMBA1002177,	HEMBA1002189,	HEMBA1002191,	HEMBA1002199,	HEMBA1002229
	HEMBA1002237,	HEMBA1002265,	HEMBA1002363,	HEMBA1002417,	HEMBA1002419,	HEMBA1002430
	HEMBA1002439,	HEMBA1002477,	HEMBA1002503,	HEMBA1002508,	HEMBA1002515,	HEMBA1002547
	HEMBA1002688,	HEMBA1002703,	HEMBA1002746,	HEMBA1002750,	HEMBA1002850,	HEMBA1002973
20	HEMBA1003021,	HEMBA1003067,	HEMBA1003077,	HEMBA1003078,	HEMBA1003079,	HEMBA1003117
	HEMBA1003129,	HEMBA1003175,	HEMBA1003199,	HEMBA1003235,	HEMBA1003250,	HEMBA1003257
	HEMBA1003291,	HEMBA1003322,	HEMBA1003327,	HEMBA1003370,	HEMBA1003380,	HEMBA1003395
	HEMBA1003402,	HEMBA1003461,	HEMBA1003480,	HEMBA1003538,	HEMBA1003545,	HEMBA1003556
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35

Group (2): 377 clones

Among the 3690 clones, the following 377 clones were full-length, and a novel clone, in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5.

HEMBA1000156, HEMBA1000231, HEMBA1000244, HEMBA1000302, HEMBA1000523, HEMBA1000531 ,
 40 HEMBA1000555, HEMBA1000568, HEMBA1000971, HEMBA1001009, HEMBA1001133, HEMBA100113 7,
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 45 HEMBA1002970, HEMBA1002971, HEMBA1002997, HEMBA1002999, HEMBA1003035, HEMBA1 003041,
 HEMBA1003433, HEMBA1003568, HEMBA1003680, HEMBA1003692, HEMBA1003804, HEMBA 1003893,
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 HEMBA1004693, HEMBA1004973, HEMBA1004977, HEMBA1005223, HEMBA1005244, HEM BA1005314,
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 50 HEMBA1006535, HEMBA1006566, HEMBA1006877, HEMBA1006936, HEMBA1007178, H EMBA1007251,
 HEMBA1007267,
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 5 NT2RM4002344, NT2RM4002452,
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 10 NT2RP2002312, NT2RP2002325, NT2RP2002503, NT2RP2002537, NT2RP2002862, NT2RP200 2925,
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50 Group (3): 1797 clones

Among the 3690 clones, the following 1797 clones were full-length, and novel clones, in which the number of the identical human ESTs for the 5'-end sequence is not more than 20 (except clones in which at least either of the 5'-end or 3'-end sequence, or both of them are not identical to any of human ESTs, and clones in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5).

55 HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000030, HEMBA1000076, HEMBA1000141,
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 55 THYRO1000288, THYRO1000320, THYRO1000327, THYRO1000358, THYRO1000394, THYRO1000 401,
 THYRO1000488, THYRO1000502, THYRO1000569, THYRO1000570, THYRO1000585, THYRO100 605,
 THYRO1000715, THYRO1000756, THYRO1000777, THYRO1000829, THYRO1000855, THYRO100 0926,
 THYRO1000983, THYRO1000984, THYRO1001120, THYRO1001134, THYRO1001173, THYRO10 01204,

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THYRO1001271, THYRO1001287, THYRO1001313, THYRO1001347, THYRO1001363, THYRO1 001405,
 THYRO1001406, THYRO1001537, THYRO1001584, THYRO1001671, THYRO1001703, THYRO 1001721,
 THYRO1001793,
 VESEN1000122, Y79AA1000013, Y79AA1000181, Y79AA1000202, Y79AA1000214, Y79AA1000230,
 5 Y79AA1000231, Y79AA1000258, Y79AA1000313, Y79AA1000328, Y79AA1000342, Y79AA100036 8,
 Y79AA1000420, Y79AA1000469, Y79AA1000480, Y79AA1000539, Y79AA1000540, Y79AA10005 60,
 Y79AA1000574, Y79AA1000589, Y79AA1000705, Y79AA1000734, Y79AA1000748, Y79AA1000 752,
 Y79AA1000774, Y79AA1000782, Y79AA1000784, Y79AA1000794, Y79AA1000800, Y79AA100 0833,
 10 Y79AA1000966, Y79AA1000968, Y79AA1001023, Y79AA1001041, Y79AA1001048, Y79AA10 01077,
 Y79AA1001078, Y79AA1001216, Y79AA1001228, Y79AA1001236, Y79AA1001312, Y79AA1 001323,
 Y79AA1001394, Y79AA1001402, Y79AA1001493, Y79AA1001511, Y79AA1001548, Y79AA 1001585,
 Y79AA1001603, Y79AA1001647, Y79AA1001665, Y79AA1001679, Y79AA1001696, Y79A A1001705,
 Y79AA1001711, Y79AA1001781, Y79AA1001805, Y79AA1001827, Y79AA1001963, Y79 AA1002027,
 Y79AA1002089, Y79AA1002093, Y79AA1002125, Y79AA1002208, Y79AA1002209, Y7 9AA1002210,
 15 Y79AA1002234, Y79AA1002258, Y79AA1002307, Y79AA1002311, Y79AA1002351, Y 79AA1002416,
 Y79AA1002487,

Group (4): 453 clones

Among the 1857 clones having the maximal ATGpr1 score not more than 0.3 (including the 9 clones whose 5'-end sequence does not contain the ATG codon), the following 453 clones were judged to be full-length since their ATGpr2 score was 0.3 or higher (Table 11). The clones were novel clones, in which at least either of the 5'-end or 3'-end sequence is not identical to any of human ESTs.

20 HEMBA1000180, HEMBA1000280, HEMBA1000282, HEMBA1000333, HEMBA1000351, HEMBA1000357,
 HEMBA1000376, HEMBA1000469, HEMBA1000504, HEMBA1000519, HEMBA1000545, HEMBA100055 7,
 25 HEMBA1000575, HEMBA1000726, HEMBA1000822, HEMBA1000934, HEMBA1000943, HEMBA10009 60,
 HEMBA1000972, HEMBA1001020, HEMBA1001051, HEMBA1001060, HEMBA1001071, HEMBA1001 208,
 HEMBA1001319, HEMBA1001383, HEMBA1001411, HEMBA1001433, HEMBA1001435, HEMBA100 1478,
 HEMBA1001522, HEMBA1001636, HEMBA1001651, HEMBA1001658, HEMBA1001709, HEMBA10 01745,
 HEMBA1001791, HEMBA1001835, HEMBA1001844, HEMBA1001888, HEMBA1001940, HEMBA1 001962,
 30 HEMBA1002022, HEMBA1002185, HEMBA1002348, HEMBA1002621, HEMBA1002645, HEMBA 1002661,
 HEMBA1002728, HEMBA1002921, HEMBA1002924, HEMBA1002934, HEMBA1002968, HEMBA1003037,
 HEMBA1003071, HEMBA1003166, HEMBA1003202, HEMBA1003204, HEMBA1003220, HEMBA1003229,
 HEMBA1003276, HEMBA1003296, HEMBA1003373, HEMBA1003531, HEMBA100364 0, HEMBA1003856,
 HEMBA1003926, HEMBA1003942, HEMBA1003987, HEMBA1004024, HEMBA10042 67, HEMBA1004323,
 35 HEMBA1004433, HEMBA1004577, HEMBA1004730, HEMBA1004778, HEMBA1004 803, HEMBA1004807,
 HEMBA1004880, HEMBA1004900, HEMBA1004983, HEMBA1005123, HEMBA100 5241, HEMBA1005311,
 HEMBA1005318, HEMBA1005353, HEMBA1005374, HEMBA1005447, HEMBA10 05588, HEMBA1005593,
 HEMBA1005606, HEMBA1005679, HEMBA1005894, HEMBA1005911, HEMBA1 006036, HEMBA1006124,
 HEMBA1006253, HEMBA1006259, HEMBA1006364, HEMBA1006380, HEMBA 1006426, HEMBA1006562,
 40 HEMBA1006597, HEMBA1006639, HEMBA1006653, HEMBA1006696, HEMB A1006744, HEMBA1006824,
 HEMBA1006949, HEMBA1007078, HEMBA1007129, HEMBA1007147, HEM BA1007206, HEMBA1007279,
 HEMBA1007327,
 HEMBB1000005, HEMBB1000055, HEMBB1000144, HEMBB1000258, HEMBB1000318, HEMBB1000335,
 HEMBB1000354, HEMBB1000374, HEMBB1000402, HEMBB1000404, HEMBB1000480, HEMBB100049 3,
 45 HEMBB1000554, HEMBB1000573, HEMBB1000649, HEMBB1000652, HEMBB1000709, HEMBB10007 49,
 HEMBB1000790, HEMBB1000827, HEMBB1000831, HEMBB1000893, HEMBB1001004, HEMBB1001 008,
 HEMBB1001047, HEMBB1001315, HEMBB1001317, HEMBB1001326, HEMBB1001367, HEMBB100 1424,
 HEMBB1001436, HEMBB1001458, HEMBB1001535, HEMBB1001565, HEMBB1001747, HEMBB10 01749,
 HEMBB1001797, HEMBB1001836, HEMBB1001863, HEMBB1001875, HEMBB1001911, HEMBB1 001922,
 50 HEMBB1001925, HEMBB1001944, HEMBB1001983, HEMBB1001996, HEMBB1001997, HEMBB 1002092,
 HEMBB1002247, HEMBB1002266, HEMBB1002387, HEMBB1002425, HEMBB1002458, HEMB B1002522,
 HEMBB1002534, HEMBB1002582, HEMBB1002596, HEMBB1002617, HEMBB1002702, MAMMA1000043,
 MAMMA1000092, MAMMA1000129, MAMMA1000198, MAMMA1000221, MAMMA1000307, MAMMA1000331,
 MAMMA1000360, MAMMA1000402, MAMMA1000414, MAMMA1000500, MAMMA100052 2, MAMMA1000576,
 55 MAMMA1000594, MAMMA1000597, MAMMA1000720, MAMMA1000775, MAMMA10007 78, MAMMA1000798,
 MAMMA1000862, MAMMA1000876, MAMMA1000931, MAMMA1000940, MAMMA1000 941, MAMMA1000975,
 MAMMA1001038, MAMMA1001186, MAMMA1001220, MAMMA1001256, MAMMA100 1274, MAMMA1001341,
 MAMMA1001397, MAMMA1001420, MAMMA1001547, MAMMA1001670, MAMMA10 01679, MAMMA1001711,

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MAMMA1001745, MAMMA1001760, MAMMA1001769, MAMMA1001815, MAMMA1 001907, MAMMA1002056, MAMMA1002078, MAMMA1002093, MAMMA1002125, MAMMA1002132, MAMMA 1002145, MAMMA1002250, MAMMA1002311, MAMMA1002411, MAMMA1002498, MAMMA1002571, MAMMA 1002701, MAMMA1002727, MAMMA1002728, MAMMA1002746, MAMMA1002764, MAMMA1002765, MAMMA1002820, MAMMA1002830, MAMMA1002909, MAMMA1002941, MAMMA1002973, MAMMA1003004, MAMMA1003007, MAMMA1003039, MAMMA1003089, NT2RM4000086, NT2RM4000265, NT2RM4000414, NT2RM4000779, NT2RM4000855, NT2RM4001160, NT2RM4001313, NT2RM4001437, NT2RM4001754, NT2RM4001953, NT2RM4001984, NT2RP2000007 7, NT2RP2000183, NT2RP2000420, NT2RP2000678, NT2RP2000715, NT2RP2000842, NT2RP20009 70, NT2RP2001149, NT2RP2001226, NT2RP2001295, NT2RP2001347, NT2RP2001569, NT2RP2001 663, NT2RP2001936, NT2RP2002041, NT2RP2002172, NT2RP2002219, NT2RP2002316, NT2RP200 2546, NT2RP2002591, NT2RP2002643, NT2RP2002741, NT2RP2002750, NT2RP2002778, NT2RP20 02857, NT2RP2003000, NT2RP2003073, NT2RP2003237, NT2RP2003394, NT2RP2003517, NT2RP2 003668, NT2RP2003988, NT2RP2004232, NT2RP2004523, NT2RP2004736, NT2RP2004767, NT2RP 2004775, NT2RP2004961, NT2RP2004962, NT2RP2004982, NT2RP2005407, NT2RP2005726, NT2R P2006258, NT2RP2006261, NT2RP2006454, NT2RP3000055, NT2RP3000233, NT2RP3000341, NT2 RP3000418, NT2RP3000451, NT2RP3000561, NT2RP3000582, NT2RP3001281, NT2RP3001339, NT 2RP3001340, NT2RP3001383, NT2RP3001432, NT2RP3001580, NT2RP3001589, NT2RP3002004, N T2RP3002173, NT2RP3003133, NT2RP3003346, NT2RP3003403, NT2RP3003576, NT2RP3003625, NT2RP3003665, NT2RP3003800, NT2RP3003828, NT2RP3004070, NT2RP3004470, NT2RP4000023, NT2RP4000035, NT2RP4000102, NT2RP4000167, NT2RP4000214, NT2RP4000218, NT2RP400042 4, NT2RP4000915, NT2RP4002075, OVARC1000085, OVARC1000092, OVARC1000145, OVARC1000414, OVARC1000496, OVARC1000526, OVARC1000948, OVARC1001011, OVARC1001600, OVARC1001805, OVARC1001813, OVARC100184 6, PLACE1000540, PLACE1000599, PLACE1001088, PLACE1001377, PLACE1001440, PLACE1001517, PLACE1001672, PLACE1001756, PLACE1002157, PLACE1002205, PLACE1002259, PLACE100239 9, PLACE1002477, PLACE1002583, PLACE1002968, PLACE1003238, PLACE1003566, PLACE10035 93, PLACE1003618, PLACE1004274, PLACE1004716, PLACE1004773, PLACE1004815, PLACE1004 979, PLACE1005052, PLACE1005086, PLACE1005128, PLACE1005176, PLACE1005467, PLACE100 5639, PLACE1005850, PLACE1006003, PLACE1006017, PLACE1006288, PLACE1006371, PLACE10 06629, PLACE1007478, PLACE1008330, PLACE1008584, PLACE1008851, PLACE1008941, PLACE1 009039, PLACE1009493, PLACE1009539, PLACE1009637, PLACE1009947, PLACE1010231, PLACE 1010562, PLACE1010579, PLACE1010739, PLACE1010802, PLACE1010896, PLACE1011032, PLAC E1011185, PLACE1011452, PLACE1011465, PLACE1011520, PLACE1011567, PLACE1011719, PLA CE2000011, PLACE2000017, PLACE2000061, PLACE2000187, PLACE2000216, PLACE2000335, PL ACE2000347, PLACE2000366, PLACE2000394, PLACE2000398, PLACE2000425, PLACE2000450, P LACE2000477, PLACE3000119, PLACE3000207, PLACE3000230, PLACE3000271, PLACE3000373, PLACE3000399, PLACE3000401, PLACE3000406, PLACE4000247, PLACE4000320, PLACE4000367, PLACE4000401, THYRO1000111, THYRO1000187, THYRO1000484, THYRO1000596, THYRO1000625, THYRO1000815, THYRO1000865, THYRO1001003, THYRO1001031, THYRO1001133, THYRO1001401, THYRO100142 6, THYRO1001434, THYRO1001559, THYRO1001570, THYRO1001706, THYRO1001746, THYRO10017 72, THYRO1001907, Y79AA1000033, Y79AA1000346, Y79AA1000805, Y79AA1001692, Y79AA1002 220,

Group (5): 24 clones

The following 24 clones having low score in the ATGpr1 were judged to be full-length since their ATGpr2 score was 0.3 or higher (Table 11). The clones were novel clones, in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5.

HEMBA1000622, HEMBA1000749, HEMBA1000876, HEMBA1001226, HEMBA1001391, HEMBA1002742, HEMBA1003908, HEMBA1004000, HEMBB1000336, MAMMA1000356, MAMMA1000883, MAMMA100159 0, NT2RP2000289, NT2RP2001467, PLACE1002853, PLACE1003420, PLACE1004836, PLACE10049 13, PLACE1006795, PLACE1008181, PLACE1008715, PLACE4000344, THYRO1000129, THYRO1001 321,

Group (6): 65 clones

The following 65 clones having low scores in both the ATGpr1 and ATGpr2 (Table 11) were judged to be full-length, since both scores were still the maximum in a cluster compared with those of the other clones(at least 2 clones or more) in the same cluster. The clones were novel clones, in which at least either of the 5'-end or 3'-end sequence is not identical to any of human ESTs.

HEMBA1000604, HEMBA1000673, HEMBA1001024, HEMBA1001026, HEMBA1001734, HEMBA1001784,

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HEMBA1001808, HEMBA1003902, HEMBA1004164, HEMBA1004909, HEMBA1005232, HEMBA100557 7,
HEMBA1006461, HEMBA1006695, HEMBB1001119, HEMBB1001337, HEMBB1001536, HEMBB10018 68,
HEMBB1002045, HEMBB1002579, MAMMA1000444, MAMMA1000761, MAMMA1000943, MAMMA1001 820,
MAMMA1002360,
5 NT2RM4000366, NT2RM4001856, NT2RM4002390, NT2RP2000108, NT2RP2000257, NT2RP2001506,
NT2RP2002047, NT2RP2002066, NT2RP2002475, NT2RP2004400, NT2RP2004587, NT2RP200528 9,
NT2RP2005694, NT2RP3001898, NT2RP3003264, NT2RP3003433, NT2RP3003842, OVARC10012 40,
PLACE1001323, PLACE1002227, PLACE1002500, PLACE1002604, PLACE1002772, PLACE1003 478,
PLACE1004681, PLACE1005108, PLACE1005932, PLACE1006318, PLACE1006368, PLACE100 6506,
10 PLACE1006904, PLACE1007557, PLACE1007877, PLACE1009048, PLACE1011109, PLACE10 11643,
PLACE4000548, THYRO1000279, Y79AA1000410, Y79AA1002103,

Group (7): 32 clones

The following 32 clones having low scores in both the ATGpr1 and ATGpr2 (Table 11) were judged to be full-length, since both scores were still the maximum in a cluster compared with those of the other clones(at least 2 clones or more) in the same cluster. The clones were novel clones, in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5.

HEMBA1000251, HEMBA1001803, HEMBA1001918, HEMBA1002257, HEMBA1003064, HEMBA1003714 ,
HEMBA1004405, HEMBA1005508, HEMBB1000054, HEMBB1001142, MAMMA1000175, MAMMA100116 2,
20 MAMMA1002972, NT2RM4000425, NT2RP2004512, NT2RP2005531, NT2RP2005942, NT2RP20065 54,
NT2RP3001007, NT2RP3001318, OVARC1000017, OVARC1000068, OVARC1000486, PLACE1001 705,
PLACE1002319, PLACE1007743, PLACE1007829, PLACE1008630, PLACE1009925, PLACE101 1492,
PLACE1011749, THYRO1000793,

The following 117 clones, selected by assembling the sequence of the other clones in the same cluster and human ESTs, have high fullness ratio. The clones were classified into the following group (8) and (9).

HEMBA1001323, HEMBA1001330, HEMBA1001712, HEMBA1001820, HEMBA1002204, HEMBA1002349,
HEMBA1002538, HEMBA1003309, HEMBA1003939, HEMBA1004015, HEMBA1004295, HEMBA100467 2,
HEMBA1004865, HEMBA1005251, HEMBA1006158, HEMBA1006676, HEMBA1006779, HEMBA10072 88,
HEMBA1000218, HEMBB1000272, HEMBB1000399, HEMBB1000491, HEMBB1000996, HEMBB1001 114,
30 HEMBB1001850, HEMBB1002015, MAMMA1000287, MAMMA1001683, MAMMA1001686, MAMMA100 2612,
NT2RM2000609, NT2RM4002438, NT2RM4002567, NT2RP2000270, NT2RP2000758, NT2RP2001290,
NT2RP2001526, NT2RP2002124, NT2RP2002736, NT2RP2002753, NT2RP2003456, NT2RP200372 7,
NT2RP2003871, NT2RP2003968, NT2RP2004321, NT2RP2004412, NT2RP2004580, NT2RP20052 93,
NT2RP2005476, NT2RP2005753, NT2RP2005815, NT2RP2005841, NT2RP2005857, NT2RP2006 393,
35 NT2RP2006467, NT2RP3000109, NT2RP3000449, NT2RP3001245, NT2RP3001634, NT2RP300 2056,
NT2RP3002810, NT2RP3002955, NT2RP3003032, NT2RP3003138, NT2RP3003500, NT2RP30 03819,
NT2RP4000078, NT2RP4000515, NT2RP4000517, NT2RP4001407, NT2RP4001889, NT2RP4 002905,
OVARC1000071, OVARC1001883, PLACE1000292, PLACE1001007, PLACE1001395, PLACE1001691 ,
PLACE1001746, PLACE1001748, PLACE1001845, PLACE1002066, PLACE1003373, PLACE100390 0,
40 PLACE1004118, PLACE1004256, PLACE1004284, PLACE1004336, PLACE1004506, PLACE10049 34,
PLACE1005077, PLACE1005111, PLACE1005409, PLACE1005730, PLACE1006076, PLACE1006 360,
PLACE1006470, PLACE1006760, PLACE1006867, PLACE1007045, PLACE1007111, PLACE100 7807,
PLACE1008080, PLACE1008244, PLACE1008369, PLACE1008405, PLACE1008426, PLACE10 08621,
PLACE1009020, PLACE1009621, PLACE1010089, PLACE1010270, PLACE3000276, THYRO1 000805,
45 THYRO1001365, THYRO1001673, Y79AA1001848,

Group (8): 36 clones

Among the 117 clones described above, the following 36 clones were novel clones, in which at least either of the 5'-end or 3'-end sequence, or both of them were not identical to any of human ESTs.

HEMBA1001330, HEMBA1001712, HEMBA1001820, HEMBA1002204, HEMBA1002349, HEMBA1003939 ,
HEMBA1004295, HEMBA1004865, HEMBA1006779, HEMBB1000218, HEMBB1000491, HEMBB100099 6,
HEMBA1001114, MAMMA1000287, MAMMA1001686, MAMMA1002612, NT2RP2002736, NT2RP20037 27,
NT2RP2004580, NT2RP2005841, NT2RP2006393, PLACE1002066, PLACE1003373, PLACE1003 900,
PLACE1004118, PLACE1004336, PLACE1004506, PLACE1004934, PLACE1005409, PLACE100 5730,
55 PLACE1006470, PLACE1008080, PLACE3000276, THYRO1000805, THYRO1001365, THYRO10 01673,

Group (9): 81 clones

Among the 117 clones described above, the following 81 clones were the clones in which the number of the identical

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human ESTs for the 5'-end sequence is not more than 20 (except clones in which at least either of the 5'-end or 3'-end sequence, or both of them are not identical to any of human ESTs, and clones in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5).

5 HEMBA1001323, HEMBA1002538, HEMBA1003309, HEMBA1004015, HEMBA1004672, HEMBA1005251, HEMBA1006158, HEMBA1006676, HEMBA1007288, HEMBB1000272, HEMBB1000399, HEMBB100185 0, HEMBB1002015, MAMMA1001683, NT2RM2000609, NT2RM4002438, NT2RM4002567, NT2RP20002 70, NT2RP2000758, NT2RP2001290, NT2RP2001526, NT2RP2002124, NT2RP2002753, NT2RP2003 456, NT2RP2003871, NT2RP2003968, NT2RP2004321, NT2RP2004412, NT2RP2005293, NT2RP200 5476, NT2RP2005753, NT2RP2005815, NT2RP2005857, NT2RP2006467, NT2RP3000109, NT2RP30 00449, 10 NT2RP3001245, NT2RP3001634, NT2RP3002056, NT2RP3002810, NT2RP3002955, NT2RP3 003032, NT2RP3003138, NT2RP3003500, NT2RP3003819, NT2RP4000078, NT2RP4000515, NT2RP 4000517, NT2RP4001407, NT2RP4001889, NT2RP4002905, OVARC1000071, OVARC1001883, PLACE1000292, PLACE1001007, PLACE1001395, PLACE1001691, PLACE1001746, PLACE1001748, PLACE1001845, PLACE1004256, PLACE1004284, PLACE100507 7, 15 PLACE1005111, PLACE1006076, PLACE1006360, PLACE1006760, PLACE1006867, PLACE10070 45, PLACE1007111, PLACE1007807, PLACE1008244, PLACE1008369, PLACE1008405, PLACE1008 426, PLACE1008621, PLACE1009020, PLACE1009621, PLACE1010089, PLACE1010270, Y79AA100 1848,

Group (10): 938 clones

20 The following 938 clones having low scores in both the ATGpr1 and ATGpr2 were judged to be full-length according to the fullness ratio shown in Table 4. The clones were novel clones, in which at least the 5'-end sequence was not identical to any of human ESTs.

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Group (11): 228 clones

The following 228 clones having low scores in both the ATGpr1 and ATGpr2 were judged to be full-length according to the fullness ratio shown in Table 7. The clones were a novel clone, in which at least the 3'-end sequence was not identical to any of human ESTs.

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EXAMPLE 12

Homology search using the 5'-end and 3'-end sequences of the selected clones.

[0172] The 5' -end sequences of the selected 5547 clones were used for the homology search of the SwissProt, and both the 5' -end 3' -end sequences were used for the search of the GenBank and UniGene (ref. the result of the search of the SwissProt, GenBank (except ESTs and STSs), and UniGene (Human) was attached).

[0173] Each search result is shown in the last part of this SPECIFICATION by arranging each item in the following format.

	5' -end sequence	3' -end sequence
Swiss-Prot	Homology search result 1	-----
GenBank	Homology search result 2	Homology search result 3
UniGene	Homology search result 4	Homology search result 5

[0174] According to the top hit data, at least 1430 clones were predicted to encode a protein belonging to any of the categories, secretory or membrane protein, glycoprotein, protein associated with signal transduction, protein associated with transcription, protein associated with diseases, enzyme or protein associated with metabolism, protein associated with cell division or cell proliferation, protein associated with cytoskeleton, protein associated with RNA synthesis, nuclear protein, protein associated with protein synthesis or transport, protein associated with cellular defense, or protein associated with development or growth. Among the clones predicted belonging to any of the categories, 1001 clones were estimated to have a relatively high homology with the known proteins or genes in the same category. In addition, 429 clones were estimated to have a relatively low homology with the known proteins in the same category.

[0175] Herein, the term "relatively high homology" is defined as having 60% or more identity and the P-value 10^{-10} or less in comparison with known sequences in the SwissProt database, or 64% or more identity and the P-value 10^{-15} or less in comparison with those in the GenBank and UniGene databases (see the attached list). Also, the term "relatively low homology" is defined as not fulfilling the requirements to be "relatively high homology", but still having the scores, 25% or more identity and the P-value 10^{-6} or less, using the sequence having 55 nucleotides or more, in comparison with known sequences in the SwissProt database (see the attached list). The P-value is a score obtained statistically by taking into account the probability of occurrence of the similarity between two sequences. In general, the smaller P-value reflects the higher similarity (Altschul S.F., Gish W., Miller W., Myers E.W., and Lipman D.J. (1990) "Basic local alignment search tool" J.Mol. Biol., 215: 403-410; Gish W., and States D.J. (1993) "Identification of protein coding regions by database similarity search" Nature Genet. 3: 266-272).

[0176] The clones predicted to encode a protein in the category of secretory protein or membrane protein have the keywords, "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen", or "connective tissue", or descriptions from which the clone can be predicted to be a secretory or membrane protein, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0177] The clones predicted to encode a protein in the category of glycoprotein have the keywords, "glycoprotein", or descriptions from which the clone can be predicted to be a glycoprotein, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0178] The clones predicted to encode a protein in the category of proteins associated with signal transduction have the keywords, "serine/threonine-protein kinase", "tyrosine-protein kinase", "SH3 domain", or "WD repeat", or descriptions from which the clone can be predicted to be a protein associated with signal transduction (such as "ADP-ribosylation factor"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0179] The clones predicted to encode a protein in the category of proteins associated with transcription have the keywords, "transcription regulation", "zinc finger", or "homeobox", or descriptions from which the clone can be predicted to be a protein associated with transcription, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0180] The clones predicted to encode a protein in the category of proteins associated with diseases are the clones in which the top hit data of the SwissProt using the 5'-end sequence, or the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence is a gene or protein that is deposited in the Online Mendelian Inheritance in Man (OMIM) database, which is a database of human genes and diseases, or the top hit data has descriptions from which the clone can be predicted to be a protein associated with diseases.

[0181] The clones predicted to encode a protein in the category of enzyme or proteins associated with metabolism are the clones in which the top hit data of the SwissProt using the 5'-end sequence, or the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence is a gene or protein with E.C.No. (Enzyme commission number), or the top hit data has descriptions from which the clone can be predicted to be an enzyme or protein associated with metabolism (such as "metabolism", "oxidoreductase", or "lipid").

[0182] The clones predicted to encode a protein in the category of proteins associated with cell division or cell proliferation have the keywords, "cell division", "cell cycle", "mitosis", or "chromosomal protein", or descriptions from which the clone can be predicted to be a protein associated with cell division or cell proliferation (such as "histone", "cell growth", or "apoptosis"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0183] The clones predicted to encode a protein in the category of proteins associated with cytoskeleton have the keywords, "structural protein", "cytoskeleton", "actin-binding", or "microtubules", or descriptions from which the clone can be predicted to be a protein associated with cytoskeleton, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0184] The clones predicted to encode a protein in the category of proteins associated with RNA synthesis include the above clones predicted to be a protein associated with transcription, and also the clones which have the keywords, "RNA splicing", or "RNA processing", or descriptions from which the clone can be predicted to be a protein associated with RNA synthesis (such as "RNA helicase", "polyadenylation", or "RNA transport"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0185] The clones predicted to encode a protein in the category of nuclear protein include the above clones predicted to be a protein associated with transcription, and also the clones which have the keyword, "nuclear protein", or descriptions from which the clone can be predicted to be a nuclear protein, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0186] The clones predicted to encode a protein in the category of proteins associated with protein synthesis or transport have the keywords, "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", or "protein transport", or descriptions from which the clone can be predicted to be a protein associated with protein synthesis or transport (such as "signal recognition particle", "ubiquitin", "proteosome", or "protease"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0187] The clones predicted to encode a protein in the category of proteins associated with cellular defense have the keywords, "heat shock", "chaperone", "DNA repair", or "DNA damage", or descriptions from which the clone can be predicted to be a protein associated with cellular defense, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0188] The clones predicted to encode a protein in the category of proteins associated with development or growth have the keyword, "developmental protein", or descriptions from which the clone can be predicted to be a protein associated with development or growth, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0189] The following 1430 clones were predicted to encode a protein belonging to any of the categories, secretory or membrane protein, glycoprotein, protein associated with signal transduction, protein associated with transcription, protein associated with diseases, enzyme or protein associated with metabolism, protein associated with cell division or cell proliferation, protein associated with cytoskeleton, protein associated with RNA synthesis, nuclear protein, protein associated with protein synthesis or transport, protein associated with cellular defense, or protein associated with development or growth.

HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000030, HEMBA1000158, HEMBA1000185, HEMBA1000201, HEMBA1000216, HEMBA1000303, HEMBA1000459, HEMBA1000488, HEMBA1000491, HEMBA1000523, HEMBA1000531, HEMBA1000542, HEMBA1000561, HEMBA1000569, HEMBA1000588, HEMBA1000591, HEMBA1000657, HEMBA1000673, HEMBA1000752, HEMBA1000827, HEMBA1000851, HEMBA1000852, HEMBA1000972, HEMBA1000991, HEMBA1001017, HEMBA1001019, HEMBA1001059, HEMBA1001071, HEMBA1001088, HEMBA1001123, HEMBA1001137, HEMBA1001174, HEMBA1001257, HEMBA1001302, HEMBA1001351, HEMBA1001387, HEMBA1001407, HEMBA1001476, HEMBA1001510, HEMBA1001569, HEMBA1001570, HEMBA1001579, HEMBA1001595, HEMBA1001620, HEMBA1001672, HEMBA1001678, HEMBA1001714, HEMBA1001744, HEMBA1001800, HEMBA1001804, HEMBA1001809, HEMBA1001819, HEMBA1001822, HEMBA1001847, HEMBA1001896, HEMBA1001913, HEMBA1001921, HEMBA1002003, HEMBA1002035, HEMBA1002092, HEMBA1002102, HEMBA1002150, HEMBA1002160, HEMBA1002161, HEMBA1002162, HEMBA1002212, HEMBA1002229, HEMBA1002257, HEMBA1002341, HEMBA1002363, HEMBA1002417, HEMBA1002495, HEMBA1002513, HEMBA1002547, HEMBA1002555, HEMBA1002569, HEMBA1002609, HEMBA1002688, HEMBA1002716, HEMBA1002810, HEMBA1002896,

	THYR01001907	F-THYR01001907	0.33
	Y79AA1000033	F-Y79AA1000033	0.53
5	Y79AA1000346	F-Y79AA1000346	0.53
	Y79AA1000410	F-Y79AA1000410	0.13
	Y79AA1000805	F-Y79AA1000805	0.32
	Y79AA1001692	F-Y79AA1001692	0.45
10	Y79AA1002103	F-Y79AA1002103	0.15
	Y79AA1002220	F-Y79AA1002220	0.49

EXAMPLE 13

Full-length sequence analysis and homology search

[0192] Full-length sequence was determined for each selected cDNA clones. The nucleotide sequence determination was performed mainly by the dye-terminator method using custom synthesized DNA primers according to the primer walking procedure (custom synthesized DNA primers were used for sequencing; sequencing reaction was performed with DNA sequencing reagent supplied by PE Biosystems according to the supplier's manual; and the samples were analyzed in an automatic sequencer made by the same supplier). Sequence determination of some clones was carried out in the same manner but using a Licor DNA sequencer. Overlapping partial nucleotide sequences, which were obtained by the above-described method, were assembled together to determine a full-length nucleotide sequence. Amino acid sequences were then deduced from the determined full-length nucleotide sequences. However, amino acid sequence is not shown for a clone of which coding region was hard to be deduced or of which amino acid sequence has less than 100 amino acid residues. SEQ ID NOs corresponding to the respective clones are indicated in Table 350 and Table 351.

[0193] GenBank, Swiss-Prot and UniGene were searched for the determined nucleotide sequences by BLAST analysis. Matching data of cDNA clone which exhibits higher homology and of which functions are easily predicted based on the nucleotide sequences and the deduced amino acid sequences are selected from the BLAST analysis matching data with P value of 10^{-4} or less. The matching data selected are listed herein. The results of homology search 6, 12, 13, and 14 are indicated in the last part of this specification. However, there are some clones that did not match the criteria for judgment and such matching data of BLAST analysis are not shown herein.

EXAMPLE 14

Novel full-length cDNA clone obtained from a cDNA library prepared by oligo-capping method

[0194] A cDNA clone, NT2RP4002298, was obtained from a cDNA library, NT2RP4 (see Example 1), prepared by oligo-capping method. Analysis of the entire nucleotide sequence of the clone has revealed that the clone encodes a novel protein consisting of 775 amino acids. The ATGpr1 score at the initiation codon of the amino acid sequence is 0.16, and therefore, the fullness ratio is low. However, the sequence can be full-length.

[0195] The full-length nucleotide sequence of NT2RP4002298 is shown in SEQ ID NO: 12370, and the deduced amino acid sequence encoded by the clone NT2RP4002298 is shown in SEQ ID NO: 12371.

EXAMPLE 15

Gene expression analysis with hybridization using high density DNA filter

[0196] Nylon membrane for DNA spotting was prepared according to the following procedure. E. coli was cultured in each well of a 96-well plate (in a LB medium at 37°C for 16 hours). A small aliquot of each culture was suspended in 10 µl of sterile water in a well of a 96-well plate. The plate was heated at 100°C for 10 minutes. Then the boiled samples were analyzed by PCR reaction. PCR was performed in a 20 µl solution by using TaKaRa PCR Amplification Kit (Takara) according to the supplier's protocol. Primers used for the amplification of an insert cDNA in a plasmid were a pair of sequencing primers, ME761FW (5' tacggaagtgttacttctgc 3' / SEQ ID NO: 13290) and ME1250RV (5' tgtgggaggttttttctcta 3' / SEQ ID NO: 13291), or a pair of primers, M13M4 (5' gtttccagtcacgac 3' / SEQ ID NO: 13292)

and M13RV (5' caggaaacagctatgac 3' / SEQ ID NO: 13293). PCR reaction was performed in a thermal cycler, GeneAmp System 9600 (PE Biosystems). The cycling profile consisted of pre-heat at 95°C for 5 minutes; 10 cycles of denaturation at 95°C for 10 seconds, and annealing/extension at 68°C for 1 minute; 20 cycles of denaturation at 98°C for 20 seconds and annealing/extension at 60°C for 3 minutes; and final extension at 72°C for 10 minutes. After the PCR reaction, the 20 µl reaction solution was loaded onto a 1 % agarose gel and fractionated by electrophoresis. DNA on the gel was stained with ethidium bromide to confirm the amplification of cDNA. When cDNAs were barely amplified by PCR, plasmids containing the corresponding insert cDNAs were prepared by the alkali-extraction method (J. Sambrook, E. F., Fritsh, & T. Maniatis, "Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989).

[0197] Preparation of DNA array was carried out by the following procedure. An Aliquot of a DNA solution was added in each well of a 384-well plate. DNA was spotted onto a nylon membrane (Boehringer) by using a 384-pin tool of Biomek 2000 Laboratory Automation Sysytem (Beckman-Coulter). Specifically, the 384-well plate containing the DNA was placed under the 384-pin tool. The independent 384 needles were simultaneously dipped into the DNA solution for DNA deposition. The needles were gently pressed onto a nylon membrane and the DNA deposited at the tips of needles was spotted onto the membrane. Denaturation of the spotted DNA and immobilization of the DNA on the nylon membrane were carried out according to usual manners (J. Sambrook, E.F., Fritsh, & T. Maniatis, "Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989).

[0198] Hybridization probe used was radioisotope-labeled 1st strand cDNA. The 1st strand cDNA synthesis was performed by using Thermoscript^(TM) RT-PCR System (GIBCO). Specifically, the 1st strand cDNA was synthesized by using 1.5 µg mRNAs from various human tissues (Clontech), 1 µl aliquots of 50 µM Oligo(dT)20 and 50 µCi [α -³²P] dATP according to an attached protocol. Probe purification was carried out by using ProbeQuant^(TM) G-50 micro column (Amersham-Pharmacia Biotech) according to an attached protocol. In the next step, 2 units of E. coli RNaseH were added to the reaction mixture. The mixture was incubated at room temperature for 10 minutes and then 100 µg of human COT-1 DNA (GIBCO) was added thereto. The mixture was incubated at 97°C for 10 minutes and then was allowed to stand on ice to give hybridization probe.

[0199] Hybridization of the radioisotope-labeled probe to the DNA array was performed in a usual manner (J. Sambrook, E.F., Fritsh, & T. Maniatis, Molecular Cloning, A laboratory manual/ 2nd edition, Cold Spring Harbor Laboratory Press, 1989). The membrane was washed as follows: the nylon membrane was incubated in Washing solution 1 (2 × SSC, 1% SDS) at room temperature (about 26°C) for 20 minutes and this washing was repeated 3 times; then the membrane was washed 3 times by incubating it in Washing solution 2 (0.1 × SSC, 1% SDS) at 65°C for 20 minutes. Autoradiography was performed by using an image plate for BAS2000 (Fuji Photo Film Co., Ltd.). Specifically, the nylon membrane with probe hybridized thereon was wrapped with a piece of Saran Wrap and brought into tight contact with the image plate on the light-sensitive surface. The membrane with the image plate was placed in an imaging cassette for radioisotope and allowed to stand in dark place for 4 hours. The radioactivity recorded on the image plate was analyzed by using BAS2000 (Fuji Photo Film Co., Ltd.). The activity was subjected to electronic conversion and recorded as an image file of autoradiogram. The signal intensity of each DNA spot was analyzed by using Visage High Density Grid Analysis Systems (Genomic Solutions Inc.). The signal intensity was converted into numerical data. The data were taken by duplicated measurements. The reproducibility was assessed by comparing the signal intensities of the corresponding spots on the duplicated DNA filters that were hybridized to a single DNA probe (Figure 2). The ratio between the corresponding spots falls within a range of 2 or less in 95% of entire spots and the correlation coefficient is $r=0.97$. Thus the reproducibility is assumed to be satisfactory.

[0200] The detection sensitivity in gene expression analysis was estimated by examining increases in the signal intensity of probe concentration-dependent spot in hybridization using a probe complementary to the DNA spotted on the nylon membrane. DNA used was PLACE1008092 (same as DNA deposited in GenBank under an Accession No. AF107253). The DNA array with DNA of PLACE1008092 was prepared according to the above-mentioned method. The probe used was prepared as follows: mRNA was synthesized in vitro from the clone, PLACE1008092. By using this mRNA as a template, radioisotope-labeled 1st strand cDNA was synthesized in the same manner as described above, and the cDNA was used as the probe. The cDNA PLACE1008092 was inserted into pBluescript SK(-), of which T7 promoter was ligated to the 5' end of the cDNA, to give a plasmid for in vitro synthesis of the mRNA from PLACE1008092. Specifically, the PLACE1008092 insert was cut out from pME18SFL3 carrying the cDNA at a DraIII site thereof by XhoI digestion. The resulting PLACE1008092 fragment was ligated to XhoI-predigested pBluescript SK (-) by using DNA ligation kit ver.2 (Takara). The in-vitro mRNA synthesis from PLACE1008092 inserted in pBluescript SK(-) was carried out by using Ampliscribe^(TM) T7 high yield transcription kit (Epicentre technologies). Hybridization and the analysis of signal intensity of each DNA spot were conducted by the same methods as described above. When the probe concentration is 1×10^7 µg/ml or less, there was no increase of signal intensity proportional to the probe concentration. Therefore it was assumed to be difficult to compare the signals with one another in the concentration range. Thus the spots with the intensity of 40 or less were indiscriminately taken as low-level signals (Figure 3). Within a concentration of the probe ranging from 1×10^7 µg/ml to 0.1 µg/ml, the signal was found to increase in a probe

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concentration-dependent manner. The detection limit was then assumed to be 1:100,000 in a ratio of mRNA expression level in a sample.

[0201] Tables 12-168 (also containing clones with no description in Examples) show the expression of each cDNA in human normal tissues (heart, lung, pituitary gland, thymus, brain, kidney, liver and spleen). The expression levels are indicated by numerical values of 0-10,000. Genes that were expressed in at least a single tissue are indicated below by the corresponding clone names:

HEMBA1000012,	HEMBA1000020,	HEMBA1000030,	HEMBA1000042,	HEMBA1000046,
HEMBA1000076,	HEMBA1000111,	HEMBA1000129,	HEMBA1000150,	HEMBA1000156,
HEMBA1000158,	HEMBA1000168,	HEMBA1000185,	HEMBA1000216,	HEMBA1000227,
HEMBA1000231,	HEMBA1000243,	HEMBA1000244,	HEMBA1000280,	HEMBA1000282,
HEMBA1000288,	HEMBA1000303,	HEMBA1000304,	HEMBA1000327,	HEMBA1000338,
HEMBA1000351,	HEMBA1000355,	HEMBA1000356,	HEMBA1000357,	HEMBA1000366,
HEMBA1000369,	HEMBA1000376,	HEMBA1000387,	HEMBA1000392,	HEMBA1000396,
HEMBA1000411,	HEMBA1000422,	HEMBA1000428,	HEMBA1000456,	HEMBA1000459,
HEMBA1000469,	HEMBA1000488,	HEMBA1000491,	HEMBA1000501,	HEMBA1000505,
HEMBA1000508,	HEMBA1000519,	HEMBA1000523,	HEMBA1000534,	HEMBA1000540,
HEMBA1000542,	HEMBA1000545,	HEMBA1000557,	HEMBA1000561,	HEMBA1000568,
HEMBA1000569,	HEMBA1000575,	HEMBA1000588,	HEMBA1000591,	HEMBA1000604,

PLACE1010891, PLACE1010896, PLACE1010916, PLACE1010917, PLACE1010960,
 PLACE1010965, PLACE1011026, PLACE1011057, PLACE1011143, PLACE1011160,
 PLACE1011165, PLACE1011203, PLACE1011214, PLACE1011221, PLACE1011229,
 PLACE1011263, PLACE1011273, PLACE1011310, PLACE1011325, PLACE1011332,
 PLACE1011375, PLACE1011399, PLACE1011419, PLACE1011433, PLACE1011465,
 PLACE1011503, PLACE1011520, PLACE1011563, PLACE1011635, PLACE1011641,
 PLACE1011643, PLACE1011664, PLACE1011675, PLACE1011729, PLACE1011762,
 PLACE1011778, PLACE1011858, PLACE1011874, PLACE1011875, PLACE1011896,
 PLACE1011964, PLACE1011982, PLACE1012031, PLACE2000006, PLACE2000014,
 PLACE2000015, PLACE2000021, PLACE2000033, PLACE2000061, PLACE2000072,
 PLACE2000097, PLACE2000115, PLACE2000136, PLACE2000164, PLACE2000223,
 PLACE2000371, PLACE2000379, PLACE2000477, PLACE3000059, PLACE3000121,
 PLACE3000160, PLACE3000199, PLACE3000218, PLACE3000244, PLACE3000310,
 PLACE3000320, PLACE3000339, PLACE3000350, PLACE3000373, PLACE4000089,
 PLACE4000093, PLACE4000147, PLACE4000252, PLACE4000270, PLACE4000367,
 PLACE4000392, PLACE4000401, PLACE4000558, PLACE4000590, PLACE4000654,
 PLACE4000670, SKNMC1000011, SKNMC1000013, SKNMC1000046, SKNMC1000050,
 SKNMC1000091, THYRO1000035, THYRO1000111, THYRO1000121, THYRO1000124,
 THYRO1000129, THYRO1000156, THYRO1000199, THYRO1000242, THYRO1000270,
 THYRO1000279, THYRO1000288, THYRO1000327, THYRO1000381, THYRO1000438,
 THYRO1000488, THYRO1000501, THYRO1000502, THYRO1000505, THYRO1000570,
 THYRO1000596, THYRO1000605, THYRO1000641, THYRO1000662, THYRO1000734,
 THYRO1000777, THYRO1000783, THYRO1000793, THYRO1000796, THYRO1000805,
 THYRO1000829, THYRO1000852, THYRO1000895, THYRO1000934, THYRO1000952,
 THYRO1001033, THYRO1001100, THYRO1001134, THYRO1001142, THYRO1001204,
 THYRO1001262, THYRO1001271, THYRO1001290, THYRO1001347, THYRO1001559,
 THYRO1001661, THYRO1001721, THYRO1001745, Y79AA1000328, Y79AA1000420,
 Y79AA1000705, Y79AA1000734, Y79AA1000748, Y79AA1000752, Y79AA1000774,
 Y79AA1000784, Y79AA1000802, Y79AA1000824, Y79AA1000827, Y79AA1000976,
 Y79AA1001078, Y79AA1001281, Y79AA1001312, Y79AA1001493, Y79AA1001541,
 Y79AA1001581, Y79AA1001585, Y79AA1001696, Y79AA1001781, Y79AA1001848,
 Y79AA1001874, Y79AA1001923, Y79AA1002027, Y79AA1002115, Y79AA1002139,
 Y79AA1002208, Y79AA1002209, Y79AA1002210, Y79AA1002220, Y79AA1002298,
 Y79AA1002307, Y79AA1002311, Y79AA1002407, Y79AA1002416, Y79AA1002431,
 Y79AA1002487.

[0204] Genes exhibiting characteristic features in the expression thereof were selected by statistical analysis of these data. Two examples are shown below to describe the selection of genes of which expression is varied greatly among tissues. The β -actin gene is used frequently as a control in gene expression analysis. Genes of which expression is varied greatly among tissues as compared that of the β -actin gene were determined as follows. Specifically, sum of squared deviation was calculated in the signal intensity of β -actin observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_a^2 . Next, sum of squared deviation was calculated in the signal intensity of a gene to be compared observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_b^2 . By taking variance ratio F as $F=S_b^2/S_a^2$, genes with a significance level of 5% or more were extracted in the F distribution. Genes extracted are indicated below by the corresponding clone names:

HEMBA1002113, HEMBA1005296, HEMBA1007121, HEMBB1000637, HEMBB1000915, MAMMA1000597, MAMMA1000605, MAMMA1000962, MAMMA1001139, MAMMA1001198, MAMMA1002858, NT2RM2001896, NT2RP2002710, NT2RP2004339, NT2RP2004538, NT2RP3000348, NT2RP3003121, PLACE3000009,

PLACE3000254, THYRO1000569, Y79AA1000131.

[0205] Gene of OVARC1000037 {heterogeneous nuclear ribonucleoprotein (hnRNP)} which expression is varied little. Genes of which expression is varied greatly among tissues as compared that of the OVARC1000037 gene were determined as follows. Specifically, sum of squared deviation was calculated in the signal intensity of β -actin observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_a^2 . Next, sum of squared deviation was calculated in the signal intensity of a gene to be compared observed in each tissue, which was divided by 7 degrees of freedom to determine a variance S_b^2 . By taking variance ratio F as $F=S_b^2/S_a^2$, genes with a significance level of 5% or more were extracted in the F distribution. Genes extracted are indicated below, by the corresponding clone names:

10	HEMBA1000304,	NT2RM2001716,	NT2RM2001840,	HEMBA1001051,	HEMBA1001109,
	OVARC1001731,	HEMBA1000726,	HEMBA1001286,	HEMBA1000387,	HEMBA1000519,
	NT2RM2001896,	HEMBA1000042,	HEMBA1001085,	HEMBA1001330,	OVARC1000576,
	HEMBA1000575,	NT2RM2000599,	NT2RM2000714,	HEMBA1000469,	NT2RM4000366,
15	HEMBA1001377,	HEMBA1000769,	HEMBA1000338,	NT2RM2000795,	HEMBA1001299,
	HEMBA1000508,	HEMBA1000150,	HEMBA1000774,	HEMBA1001226,	HEMBA1000960,
	NT2RM4000795,	HEMBA1002162,	NT2RM4001876,	NT2RM4002482,	HEMBA1001678,
	HEMBA1002113,	NT2RM4002383,	HEMBA1002229,	HEMBA1002818,	HEMBA1001454,
20	NT2RM4000764,	HEMBA1001510,	HEMBA1001714,	HEMBA1002150,	NT2RM4002044,
	HEMBA1002728,	NT2RM4002189,	HEMBA1001991,	HEMBA1002166,	NT2RM4002499,
	NT2RM4001140,	NT2RM4002504,	HEMBA1002590,	HEMBA1001435,	PLACE1000706,
	HEMBA1002160,	HEMBA1001824,	HEMBA1001463,	HEMBA1001533,	HEMBA1001570,
25	PLACE1001036,	HEMBA1001651,	HEMBA1002381,	HEMBA1002934,	HEMBA1003370,
	HEMBA1003021,	HEMBA1003166,	NT2RP1000738,	NT2RP2000040,	HEMBA1004164,
	HEMBA1003836,	HEMBA1004267,	NT2RP2000845,	HEMBA1003041,	HEMBA1003571,
	HEMBA1003758,	NT2RP2000108,	HEMBA1003838,	NT2RP1000357,	HEMBA1003376,
30	PLACE1003528,	HEMBA1003528,	NT2RP1001475,	HEMBA1004049,	HEMBA1003212,
	HEMBA1003667,	PLACE1004149,	HEMBA1003926,	HEMBA1004306,	HEMBA1004024,
	NT2RP1000363,	HEMBA1003033,	HEMBA1004335,	HEMBA1003348,	HEMBA1003034,
	NT2RP2001081,	HEMBA1004056,	HEMBA1003314,	HEMBA1003827,	HEMBA1003893,
35	NT2RP2001036,	NT2RP2001168,	NT2RP2001328,	HEMBA1005035,	NT2RP2001569,
	NT2RP2002439,	HEMBA1005511,	HEMBA1005999,	NT2RP2002862,	NT2RP2002979,
	NT2RP2001394,	HEMBA1004753,	NT2RP2002621,	HEMBA1005853,	HEMBA1005443,
	NT2RP2002980,	NT2RP2001347,	HEMBA1005241,	NT2RP2002750,	NT2RP2003533,
40	HEMBA1005634,	NT2RP2003034,	HEMBA1006138,	NT2RP2003117,	NT2RP2001366,
	HEMBA1005079,	NT2RP2003293,	NT2RP2002710,	HEMBA1005911,	NT2RP2002752,
	HEMBA1006036,	NT2RP2002987,	HEMBA1006100,	HEMBA1004460,	HEMBA1004538,
	NT2RP2001943,	NT2RP2002033,	HEMBA1005296,	HEMBA1005829,	HEMBA1005520,
45	HEMBA1005123,	HEMBA1005552,	HEMBA1004930,	NT2RP2001312,	HEMBA1005304,
	HEMBA1005834,	HEMBA1005990,	HEMBA1005526,	NT2RP2003073,	HEMBA1005331,
	HEMBA1006744,	HEMBA1006780,	NT2RP2004339,	HEMBA1000173,	HEMBA1007113,
50	NT2RP2005908,	HEMBA1000376,	HEMBA1000024,	HEMBA1000510,	NT2RP2004580,

55

MAMMA1002428, MAMMA1002590, MAMMA1001186, MAMMA1002267, MAMMA1002322,
 MAMMA1001956, MAMMA1002155, NT2RP4000210, MAMMA1002622, NT2RP3004125,
 5 MAMMA1001220, MAMMA1001683, NT2RP3004348, Y79AA1000214, Y79AA1000833,
 NT2RP4000212, MAMMA1002230, MAMMA1001452, MAMMA1001620, MAMMA1001256,
 MAMMA1001760, NT2RP3004349, MAMMA1001783, MAMMA1001907, MAMMA1002009,
 MAMMA1002545, NT2RP4000214, NT2RP4000728, MAMMA1001465, MAMMA1001154,
 10 MAMMA1001198, MAMMA1001343, MAMMA1002310, NT2RP4000035, NT2RP4000833,
 MAMMA1003150, MAMMA1002886, NT2RP4001938, NT2RM2000260, MAMMA1002629,
 MAMMA1002973, MAMMA1002721, MAMMA1002909, NT2RP4001100, NT2RM1000857,
 NT2RP4000878, MAMMA1002844, NT2RM1000039, NT2RP4001174, MAMMA1002665,
 15 MAMMA1003047, NT2RM1000086, NT2RM1000260, NT2RM1000355, MAMMA1002701,
 NT2RP4000918, MAMMA1002830, MAMMA1002970, NT2RP4001677, NT2RM2000422,
 MAMMA1003004, MAMMA1002673, MAMMA1003031, MAMMA1002764, MAMMA1002858,
 NT2RP4001679, NT2RP4002888, MAMMA1002711, NT2RP4001276, NT2RM1000018,
 20 NT2RP4001568, NT2RM1000883.

[0206] Thus, characteristic features in the expression of a gene are illustrated by comparing and _ statistically analyzing the expression of many genes.

25 Analysis of disease-associated genes

[0207] Non-enzymic protein glycation reaction is believed to be a cause of a variety of chronic diabetic complications. Accordingly, genes of which expression is elevated or decreased in a glycated protein-specific manner in the endothelial cells are associated with diabetic complications caused by glycated proteins. Vascular endothelial cells are affected with glycated proteins present in blood. Reaction products of non-enzymic protein glycation include amadori compound (glycated protein) as a mildly glycated protein and advanced glycation endproduct as a heavily glycated protein. Hence, a survey was carried out for genes of which expression levels are varied depending on the presence of these glycated proteins in endothelial cells. The mRNAs were extracted from endothelial cells that were cultured in the presence or absence of glycated protein. The mRNAs were converted into radiolabeled first strand cDNAs for preparing probes. 30 The probes were hybridized to the above-mentioned DNA array. Signal of each DNA spot was detected by BAS2000 and analyzed by ArrayGauge (Fuji Photo Film Co., Ltd.).

[0208] Advanced glycation endproduct of bovine serum albumin was prepared as follows: bovine serum albumin (BSA; Sigma) was incubated in a phosphate buffer solution containing 50 mM glucose at 37°C for 8 weeks; and the resulting brownish BSA was dialyzed against a phosphate buffer solution.

40 **[0209]** Human normal pulmonary arterial endothelial cells (Cell Applications) were cultured in an Endothelial Cell Growth Medium (Cell Applications). The culture dish (Farcon) with the cells were incubated in a CO₂ incubator (37°C, 5% CO₂, in a humid atmosphere). When the cells were grown to be confluent in the dish, 250 µg/ml of bovine serum albumin (sigma), glycated bovine serum albumin (Sigma) or advanced glycation endproduct of bovine serum albumin was added thereto and the cells were incubated for 33 hours. The mRNA was extracted from the cells by using a FastTackTM 2.0 kit (Invitrogen). The labeling of hybridization probe was carried out by using the mRNA according to 45 the same procedure as described above.

[0210] Table 169 shows the expression level of each cDNA in human pulmonary arterial endothelial cells cultured in a medium containing bovine serum albumin (sigma), glycated bovine serum albumin (Sigma) or advanced glycation endproduct of bovine serum albumin. Genes of which expression was detected in the endothelial cell are as follows: 50

Y79AA1000850, Y79AA1000966, Y79AA1000968, Y79AA1000985, Y79AA1001061,
 Y79AA1001068, Y79AA1001077, Y79AA1001078, Y79AA1001105, Y79AA1001145,
 5 Y79AA1001211, Y79AA1001216, Y79AA1001228, Y79AA1001236, Y79AA1001299,
 Y79AA1001394, Y79AA1001402, Y79AA1001511, Y79AA1001533, Y79AA1001548,
 Y79AA1001555, Y79AA1001581, Y79AA1001585, Y79AA1001603, Y79AA1001647,
 Y79AA1001665, Y79AA1001679, Y79AA1001711, Y79AA1001805, Y79AA1001827,
 10 Y79AA1001846, Y79AA1001866, Y79AA1001875, Y79AA1001923, Y79AA1001963,
 Y79AA1002089, Y79AA1002093, Y79AA1002115, Y79AA1002125, Y79AA1002209,
 Y79AA1002211, Y79AA1002220, Y79AA1002246, Y79AA1002258, Y79AA1002311,
 Y79AA1002351, Y79AA1002361, Y79AA1002472, Y79AA1002482

15 **[0211]** Signal ratios of EC_AGE_BSA to EC_BSA and of EC_glycated_BSA to EC_BSA were calculated for each gene. Genes with high signal ratios were selected. In the case of calculating the ratio of signal value of 40 or less to that of more than 40, such signal values were, for convenience, taken as 40 instead of the real values. When the ratio EC_AGE_BSA/EC_BSA is 2 or more, expression of the genes exhibiting such ratio is expected to be elevated due to advanced glycation endproduct of bovine serum albumin. The higher the value is, the higher the gene expression level is. When the ratio EC_AGE_BSA/EC_BSA ranges from 0.5 to 2, expression of the genes exhibiting such ratio is expected to be unaffected due to advanced glycation endproduct of bovine serum albumin. When the ratio EC_AGE_BSA/EC_BSA is less than 0.5, expression of the genes exhibiting such ratio value is expected to be decreased due to advanced glycation endproduct of bovine serum albumin. The lower the value is, the lower the gene expression level is.

20 **[0212]** Clone with EC_AGE_BSA/EC_BSA ratio of 2 or higher are as follows: HEMBA1003958, MAMMA1001256, PLACE2000411.

[0213] Clone with EC_AGE_BSA/EC_BSA ratio of 0.5 or less is as follows: MAMMA1001783. These cDNAs are associated with diabetes.

[0214] When the ratio EC_glycated_BSA/EC_BSA is 2 or more, the expression level of the gene exhibiting such ratio is expected to be elevated due to glycated bovine serum albumin. The higher the value is, the higher the gene expression level is. When the ratio EC_glycated_BSA/EC_BSA ranges from 0.5 to 2, the expression level of the gene exhibiting such ratio is expected to be unaffected with glycated bovine serum albumin. When the ratio EC_glycated_BSA/EC_BSA is less than 0.5, the expression level of a gene exhibiting such ratio is expected to be decreased due to glycated bovine serum albumin. The lower the value is, the lower the gene expression level is.

35 **[0215]** Clones with EC_glycated_BSA/EC_BSA ratio of 2 or more are as follows: HEMBA1004850, MAMMA1001256, MAMMA1002132 and PLACE3000119.

[0216] A clone with EC_glycated_BSA/EC_BSA ratio of 0.5 or less is as follows: MAMMA1001783.

[0217] These cDNAs are also associated with diabetes.

40 Analysis of genes associated with neural cell differentiation

[0218] Genes involved in neural cell differentiation are useful for treating neurological diseases. It is possible that genes with varying expression levels in response to induction of cellular differentiation in neural cells are associated with neurological diseases.

45 **[0219]** A survey was performed for genes of which expression levels are varied in response to induction of differentiation (stimulation by retinoic acid (RA)) in cultured cells of a neural strain, NT2.

[0220] The NT2 cells were treated basically according to supplier's instruction manual. "Undifferentiated NT2 cells" means NT2 cells successively cultured in an Opti-MEM I (GIBCO-BRL; catalog No. 31985) containing 10%(v/v) fetal bovine serum and 1%(v/v) penicillin-streptomycin (GIBCO BRL). "NT2 cells cultured in the presence of retinoic acid" means the cells resulted from transferring undifferentiated NT2 cells into a retinoic acid-containing medium, which consists of D-MEM (GIBCO BRL; catalog No. 11965), 10%(v/v) fetal bovine serum, 1%(v/v) penicillin-streptomycin and 10 μ M retinoic acid (GIBCO-BRL), and the subsequent successive culture therein for 5 weeks. "NT2 cells that were cultured in the presence of retinoic acid and then further cultured in the presence of cell-division inhibitor added" means 55 NT2 cells resulted from transferring NT2 cells cultured in the presence of retinoic acid for 5 weeks into a cell-division inhibitor-containing medium, which consisted of D-MEM(GIBCO BRL; catalog No.11965), 10%(v/v) fetal bovine serum, 1%(v/v) penicillin-streptomycin, 10 μ M retinoic acid, 10 μ M FudR (5-fluoro-2'-deoxyuridine: GIBCO BRL), 10 μ M Urd (Uridine: GIBCO BRL) and 1 μ M araC (Cytosine β -D-Arabinofuranoside: GIBCO BRL), and the subsequence succes-

sive culture for 2 weeks. Each of the cells were treated with trypsin and then harvested. Total RNAs were extracted from the cells by using S.N.A.P.^(TM) Total RNA Isolation kit (Invitrogen^(d)). The labeling of probe used for hybridization was carried out by using 10 µg of the total RNA according to the same methods as described above. The data were obtained in triplicate (n=3). The data of signal value representing gene expression level in the cells in the presence of stimulation for inducing differentiation were compared with those in the absence of the stimulation. The comparison was performed by statistical treatment-of two-sample t-test. Clones with significant difference in the signal distribution were selected under the condition of $p < 0.05$. In this analysis, clones with the difference can be statistically detected even when the signals were low. Accordingly, clones with signal value of 40 or less were also assessed for the selection. [0221] Tables 170-349 show the expression level of each cDNA in undifferentiated NT2 cells, NT2 cells cultured in the presence of RA, and NT2 cells that were cultured in the presence of RA and that were further cultured in the presence of cell-division inhibitor added.

[0222] Averaged signal values (M_1 , M_2) and sample variances (s_1^2 , s_2^2) were calculated for each gene in each of the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells to be compared. The t values were determined according to the following formula: $t = (M_1 - M_2) / s / ((1/3 + 1/3)^{1/2})$. When the determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01 in the t-distribution table with 4 degrees of freedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p < 0.05$ or $p < 0.01$, respectively. The tables also include the information on an increase (+) or decrease (-) in the expression level of a gene in the treated cells when the level is compared with that of untreated undifferentiated cells.

[0223] Clones of which expression levels increased by RA are as follows:

HEMBA1000005,	HEMBA1000042,	HEMBA1000046,	HEMBA1000076,	HEMBA1000111,	HEMBA1000141,
HEMBA1000150,	HEMBA1000185,	HEMBA1000282,	HEMBA1000304,	HEMBA1000307,	HEMBA1000338,
HEMBA1000357,	HEMBA1000376,	HEMBA1000387,	HEMBA1000392,	HEMBA1000428,	HEMBA1000456,
HEMBA1000459,	HEMBA1000469,	HEMBA1000504,	HEMBA1000508,	HEMBA1000519,	HEMBA1000540,
HEMBA1000545,	HEMBA1000557,	HEMBA1000563,	HEMBA1000568,	HEMBA1000575,	HEMBA1000588,
HEMBA1000592,	HEMBA1000604,	HEMBA1000622,	HEMBA1000655,	HEMBA1000673,	HEMBA1000682,
HEMBA1000726,	HEMBA1000727,	HEMBA1000749,	HEMBA1000769,	HEMBA1000774,	HEMBA1000791,
HEMBA1000822,	HEMBA1000872,	HEMBA1000876,	HEMBA1000910,	HEMBA1000942,	HEMBA1000943,
HEMBA1000960,	HEMBA1000972,	HEMBA1000974,	HEMBA1000991,	HEMBA1001008,	HEMBA1001020,
HEMBA1001043,	HEMBA1001051,	HEMBA1001060,	HEMBA1001071,	HEMBA1001077,	HEMBA1001085,
HEMBA1001094,	HEMBA1001109,	HEMBA1001121,	HEMBA1001122,	HEMBA1001140,	HEMBA1001172,
HEMBA1001226,	HEMBA1001235,	HEMBA1001265,	HEMBA1001281,	HEMBA1001294,	HEMBA1001299,
HEMBA1001319,	HEMBA1001323,	HEMBA1001330,	HEMBA1001351,	HEMBA1001361,	HEMBA1001377,
HEMBA1001388,	HEMBA1001391,	HEMBA1001398,	HEMBA1001432,	HEMBA1001435,	HEMBA1001442,
HEMBA1001454,	HEMBA1001455,	HEMBA1001497,	HEMBA1001517,	HEMBA1001569,	HEMBA1001570,
HEMBA1001581,	HEMBA1001585,	HEMBA1001620,	HEMBA1001711,	HEMBA1001718,	HEMBA1001723,
HEMBA1001761,	HEMBA1001815,	HEMBA1001819,	HEMBA1001861,	HEMBA1001864,	HEMBA1001869,
HEMBA1001888,	HEMBA1001915,	HEMBA1001918,	HEMBA1001940,	HEMBA1001964,	HEMBA1001967,
HEMBA1001979,	HEMBA1001987,	HEMBA1001991,	HEMBA1002008,	HEMBA1002022,	HEMBA1002039,
HEMBA1002049,	HEMBA1002084,	HEMBA1002102,	HEMBA1002113,	HEMBA1002144,	HEMBA1002160,
HEMBA1002162,	HEMBA1002185,	HEMBA1002212,	HEMBA1002226,	HEMBA1002229,	HEMBA1002267,
HEMBA1002270,	HEMBA1002337,	HEMBA1002381,	HEMBA1002458,	HEMBA1002477,	HEMBA1002508,
HEMBA1002558,	HEMBA1002561,	HEMBA1002583,	HEMBA1002590,	HEMBA1002628,	HEMBA1002645,
HEMBA1002661,	HEMBA1002678,	HEMBA1002712,	HEMBA1002728,	HEMBA1002780,	HEMBA1002850,
HEMBA1002886,	HEMBA1002934,	HEMBA1002935,	HEMBA1002939,	HEMBA1002951,	HEMBA1002968,
HEMBA1002970,	HEMBA1002973,	HEMBA1002999,	HEMBA1003021,	HEMBA1003033,	HEMBA1003034,
HEMBA1003064,	HEMBA1003067,	HEMBA1003078,	HEMBA1003086,	HEMBA1003096,	HEMBA1003129,
HEMBA1003142,	HEMBA1003148,	HEMBA1003166,	HEMBA1003175,	HEMBA1003197,	HEMBA1003199,
HEMBA1003202,	HEMBA1003204,	HEMBA1003212,	HEMBA1003235,	HEMBA1003250,	HEMBA1003273,
HEMBA1003276,	HEMBA1003278,	HEMBA1003291,	HEMBA1003309,	HEMBA1003322,	HEMBA1003328,
HEMBA1003348,	HEMBA1003369,	HEMBA1003376,	HEMBA1003384,	HEMBA1003395,	HEMBA1003463,
HEMBA1003480,	HEMBA1003531,	HEMBA1003548,	HEMBA1003591,	HEMBA1003595,	HEMBA1003597,
HEMBA1003617,	HEMBA1003621,	HEMBA1003622,	HEMBA1003637,	HEMBA1003640,	HEMBA1003645,
HEMBA1003646,	HEMBA1003656,	HEMBA1003679,	HEMBA1003692,	HEMBA1003715,	HEMBA1003720,
HEMBA1003725,	HEMBA1003729,	HEMBA1003758,	HEMBA1003803,	HEMBA1003805,	HEMBA1003836,
HEMBA1003838,	HEMBA1003879,	HEMBA1003885,	HEMBA1003893,	HEMBA1003908,	HEMBA1003937,
HEMBA1003942,	HEMBA1003953,	HEMBA1003958,	HEMBA1003959,	HEMBA1003978,	HEMBA1003987,
HEMBA1003989,	HEMBA1004000,	HEMBA1004011,	HEMBA1004012,	HEMBA1004015,	HEMBA1004024,

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5	HEMBA1004049,	HEMBA1004056,	HEMBA1004111,	HEMBA1004132,	HEMBA1004143,	HEMBA1004164,
	HEMBA1004199,	HEMBA1004200,	HEMBA1004207,	HEMBA1004225,	HEMBA1004246,	HEMBA1004248,
	HEMBA1004267,	HEMBA1004289,	HEMBA1004312,	HEMBA1004323,	HEMBA1004335,	HEMBA1004353,
	HEMBA1004354,	HEMBA1004356,	HEMBA1004366,	HEMBA1004396,	HEMBA1004405,	HEMBA1004429,
	HEMBA1004433,	HEMBA1004460,	HEMBA1004499,	HEMBA1004502,	HEMBA1004506,	HEMBA1004534,
10	HEMBA1004538,	HEMBA1004573,	HEMBA1004577,	HEMBA1004586,	HEMBA1004610,	HEMBA1004629,
	HEMBA1004666,	HEMBA1004669,	HEMBA1004672,	HEMBA1004709,	HEMBA1004733,	HEMBA1004736,
	HEMBA1004748,	HEMBA1004751,	HEMBA1004758,	HEMBA1004763,	HEMBA1004768,	HEMBA1004770,
	HEMBA1004778,	HEMBA1004803,	HEMBA1004820,	HEMBA1004847,	HEMBA1004863,	HEMBA1004880,
	HEMBA1004909,	HEMBA1004918,	HEMBA1004923,	HEMBA1004930,	HEMBA1004934,	HEMBA1004944,
15	HEMBA1004954,	HEMBA1004980,	HEMBA1005035,	HEMBA1005039,	HEMBA1005075,	HEMBA1005079,
	HEMBA1005113,	HEMBA1005123,	HEMBA1005133,	HEMBA1005149,	HEMBA1005152,	HEMBA1005219,
	HEMBA1005223,	HEMBA1005232,	HEMBA1005251,	HEMBA1005274,	HEMBA1005275,	HEMBA1005304,
	HEMBA1005311,	HEMBA1005314,	HEMBA1005359,	HEMBA1005367,	HEMBA1005374,	HEMBA1005410,
	HEMBA1005411,	HEMBA1005423,	HEMBA1005426,	HEMBA1005443,	HEMBA1005447,	HEMBA1005474,
20	HEMBA1005508,	HEMBA1005511,	HEMBA1005520,	HEMBA1005526,	HEMBA1005548,	HEMBA1005552,
	HEMBA1005576,	HEMBA1005581,	HEMBA1005582,	HEMBA1005583,	HEMBA1005588,	HEMBA1005595,
	HEMBA1005609,	HEMBA1005616,	HEMBA1005627,	HEMBA1005631,	HEMBA1005666,	HEMBA1005670,
	HEMBA1005679,	HEMBA1005699,	HEMBA1005705,	HEMBA1005765,	HEMBA1005780,	HEMBA1005822,
	HEMBA1005829,	HEMBA1005834,	HEMBA1005853,	HEMBA1005891,	HEMBA1005894,	HEMBA1005911,
25	HEMBA1005921,	HEMBA1005991,	HEMBA1005999,	HEMBA1006036,	HEMBA1006042,	HEMBA1006100,
	HEMBA1006138,	HEMBA1006142,	HEMBA1006268,	HEMBA1006278,	HEMBA1006328,	HEMBA1006344,
	HEMBA1006359,	HEMBA1006398,	HEMBA1006416,	HEMBA1006419,	HEMBA1006421,	HEMBA1006426,
	HEMBA1006438,	HEMBA1006483,	HEMBA1006485,	HEMBA1006502,	HEMBA1006507,	HEMBA1006546,
	HEMBA1006559,	HEMBA1006562,	HEMBA1006579,	HEMBA1006597,	HEMBA1006612,	HEMBA1006617,
30	HEMBA1006631,	HEMBA1006635,	HEMBA1006652,	HEMBA1006695,	HEMBA1006744,	HEMBA1006754,
	HEMBA1006779,	HEMBA1006780,	HEMBA1006795,	HEMBA1006821,	HEMBA1006865,	HEMBA1006926,
	HEMBA1006973,	HEMBA1007017,	HEMBA1007052,	HEMBA1007080,	HEMBA1007085,	HEMBA1007113,
	HEMBA1007121,	HEMBA1007147,	HEMBA1007149,	HEMBA1007206,	HEMBA1007224,	HEMBA1007256,
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
35	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
40	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
45	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,	HEMBA1007327,	HEMBA1007341,	HEMBA1007347,	
	HEMBA1007267,	HEMBA1007288,				

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	MAMMA1000009,	MAMMA1000043,	MAMMA1000045,	MAMMA1000084,	MAMMA1000103,	MAMMA1000134,
	MAMMA1000139,	MAMMA1000143,	MAMMA1000171,	MAMMA1000241,	MAMMA1000251,	MAMMA1000254,
	MAMMA1000257,	MAMMA1000264,	MAMMA1000266,	MAMMA1000270,	MAMMA1000279,	MAMMA1000287,
	MAMMA1000340,	MAMMA1000348,	MAMMA1000360,	MAMMA1000361,	MAMMA1000372,	MAMMA1000385,
5	MAMMA1000402,	MAMMA1000424,	MAMMA1000478,	MAMMA1000500,	MAMMA1000522,	MAMMA1000524,
	MAMMA1000565,	MAMMA1000567,	MAMMA1000576,	MAMMA1000585,	MAMMA1000594,	MAMMA1000597,
	MAMMA1000605,	MAMMA1000616,	MAMMA1000643,	MAMMA1000664,	MAMMA1000669,	MAMMA1000696,
	MAMMA1000718,	MAMMA1000723,	MAMMA1000731,	MAMMA1000744,	MAMMA1000746,	MAMMA1000752,
	MAMMA1000760,	MAMMA1000761,	MAMMA1000776,	MAMMA1000802,	MAMMA1000824,	MAMMA1000839,
10	MAMMA1000880,	MAMMA1000905,	MAMMA1000931,	MAMMA1000940,	MAMMA1000941,	MAMMA1000943,
	MAMMA1000957,	MAMMA1000962,	MAMMA1000968,	MAMMA1000987,	MAMMA1000998,	MAMMA1001003,
	MAMMA1001035,	MAMMA1001038,	MAMMA1001067,	MAMMA1001078,	MAMMA1001092,	MAMMA1001126,
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	PLACE4000558,	PLACE4000581,	PLACE4000650,	PLACE4000654,		
20	THYRO1000034,	THYRO1000085,	THYRO1000092,	THYRO1000111,	THYRO1000156,	THYRO1000163,
	THYRO1000173,	THYRO1000190,	THYRO1000197,	THYRO1000221,	THYRO1000241,	THYRO1000327,
	THYRO1000381,	THYRO1000387,	THYRO1000394,	THYRO1000488,	THYRO1000585,	THYRO1000625,
	THYRO1000637,	THYRO1000658,	THYRO1000666,	THYRO1000676,	THYRO1000684,	THYRO1000712,
	THYRO1000734,	THYRO1000793,	THYRO1000796,	THYRO1000805,	THYRO1000815,	THYRO1000865,
25	THYRO1000916,	THYRO1000934,	THYRO1000974,	THYRO1000975,	THYRO1001031,	THYRO1001062,
	THYRO1001093,	THYRO1001133,	THYRO1001173,	THYRO1001177,		
	THYRO1001189,	THYRO1001204,	THYRO1001213,	THYRO1001262,	THYRO1001290,	THYRO1001320,
	THYRO1001322,	THYRO1001401,	THYRO1001406,	THYRO1001426,	THYRO1001480,	THYRO1001487,
	THYRO1001537,	THYRO1001595,	THYRO1001617,	THYRO1001637,	THYRO1001706,	THYRO1001772,
30	THYRO1001828,	THYRO1001854,	Y79AA1000059,	Y79AA1000214,	Y79AA1000355,	Y79AA1000410,
	Y79AA1000538,	Y79AA1000539,	Y79AA1000705,	Y79AA1000800,	Y79AA1000850,	Y79AA1000962,
	Y79AA1000976,	Y79AA1001061,	Y79AA1001068,	Y79AA1001493,	Y79AA1001548,	Y79AA1001585,
	Y79AA1001594,	Y79AA1001696,	Y79AA1001711,	Y79AA1002103,	Y79AA1002115,	Y79AA1002258,
	Y79AA1002361,	Y79AA1002407,	Y79AA1002472,	Y79AA1002482,		
35	[0224] Clones of which expression levels decreased by RA are as follows:					
	HEMBA1000946,	HEMBA1003569,	HEMBA1005570,	HEMBA1000915,	NT2RM1000666,	NT2RM2000092,
	NT2RM2000594,	NT2RM2001256,	NT2RM4001754,	NT2RM4001905,	NT2RP2001675,	NT2RP2002047,
	NT2RP2005491,	NT2RP3000980,	NT2RP3002081,	NT2RP3004594,	NT2RP4001950,	NT2RP4002408,
	OVARC1000431,	OVARC1001942,	OVARC1001943,	PLACE1003190,	PLACE1004868,	PLACE1005923,
40	PLACE1007257,	PLACE1010624,	Y79AA1000346,			
	[0225] Clones of which expression levels increase by RA/inhibitor are as follows:					
	HEMBA1000046,	HEMBA1000307,	HEMBA1000434,	HEMBA1000504,	HEMBA1000588,	HEMBA1000682,
	HEMBA1000726,	HEMBA1000943,	HEMBA1001071,	HEMBA1001094,	HEMBA1001122,	HEMBA1001323,
	HEMBA1001361,	HEMBA1001455,	HEMBA1001709,	HEMBA1001746,	HEMBA1001869,	HEMBA1002084,
45	HEMBA1002583,	HEMBA1002628,	HEMBA1002801,	HEMBA1002937,	HEMBA1003096,	HEMBA1003142,
	HEMBA1003229,	HEMBA1003276,	HEMBA1003309,	HEMBA1003463,	HEMBA1003597,	HEMBA1003617,
	HEMBA1003725,	HEMBA1003803,	HEMBA1003879,	HEMBA1003989,	HEMBA1004000,	HEMBA1004015,
	HEMBA1004024,	HEMBA1004049,	HEMBA1004056,	HEMBA1004199,	HEMBA1004248,	HEMBA1004356,
	HEMBA1004554,	HEMBA1004666,	HEMBA1004725,	HEMBA1004770,	HEMBA1004803,	HEMBA1004923,
50	HEMBA1004934,	HEMBA1004954,	HEMBA1005039,	HEMBA1005075,	HEMBA1005113,	HEMBA1005219,
	HEMBA1005232,	HEMBA1005251,	HEMBA1005304,	HEMBA1005367,	HEMBA1005372,	HEMBA1005403,
	HEMBA1005410,	HEMBA1005411,	HEMBA1005548,	HEMBA1005581,	HEMBA1005631,	HEMBA1005666,
	HEMBA1005755,	HEMBA1005780,	HEMBA1006067,	HEMBA1006130,	HEMBA1006364,	HEMBA1006485,
	HEMBA1006559,	HEMBA1006579,	HEMBA1006754,	HEMBA1000059,	HEMBA1000575,	HEMBA1000709,
55	HEMBA1000822,	HEMBA1000848,	HEMBA1000852,	HEMBA1000913,	HEMBA1000985,	HEMBA1001117,
	HEMBA1001210,	HEMBA1001317,	HEMBA1001394,	HEMBA1001443,	HEMBA1001668,	HEMBA1001695,
	HEMBA1002049,	HEMBA1002254,	HEMBA1002266,	HEMBA1002371,	HEMBA1002502,	HEMBA1002614,
	HEMBA1002617,	HEMBA1002692,	HEMBA1002697,	MAMMA1000241,	MAMMA1000424,	MAMMA1000616,

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	MAMMA1000731,	MAMMA1000824,	MAMMA1000908,	MAMMA1000956,	MAMMA1001038,	MAMMA1001091,
	MAMMA1001243,	MAMMA1001815,	MAMMA1001820,	MAMMA1002267,	MAMMA1002769,	MAMMA1002871,
	MAMMA1002941,	NT2RM1000355,	NT2RM1000725,	NT2RM1000829,	NT2RM1000850,	NT2RM1000898,
	NT2RM2000504,	NT2RM2000635,	NT2RM2000718,	NT2RM2000821,	NT2RM2001370,	NT2RM2001582,
5	NT2RM2001592,	NT2RM2001613,	NT2RM2001632,	NT2RM2001635,	NT2RM2001648,	NT2RM2001659,
	NT2RM2001671,	NT2RM2001695,	NT2RM2001760,	NT2RM2001782,	NT2RM2001839,	NT2RM2001879,
	NT2RM2001983,	NT2RM4000104,	NT2RM4000290,	NT2RM4000425,	NT2RM4000433,	NT2RM4000471,
	NT2RM4000531,	NT2RM4000852,	NT2RM4001047,	NT2RM4001347,	NT2RM4001454,	NT2RM4001557,
	NT2RM4001566,	NT2RM4001582,	NT2RM4001938,	NT2RM4001953,	NT2RM4002018,	NT2RM4002409,
10	NT2RM4002558,	NT2RM4002594,	NT2RP1000259,	NT2RP1000418,	NT2RP1000574,	NT2RP1000629,
	NT2RP1000782,	NT2RP1000856,	NT2RP1000943,	NT2RP1000988,	NT2RP1001013,	NT2RP1001173,
	NT2RP1001546,	NT2RP2000091,	NT2RP2000208,	NT2RP2000274,	NT2RP2000329,	NT2RP2000369,
	NT2RP2000634,	NT2RP2000842,	NT2RP2000943,	NT2RP2000987,	NT2RP2001094,	NT2RP2001277,
	NT2RP2001290,	NT2RP2001366,	NT2RP2001423,	NT2RP2001436,	NT2RP2001467,	NT2RP2001506,
15	NT2RP2001601,	NT2RP2001663,	NT2RP2001926,	NT2RP2001985,	NT2RP2002032,	NT2RP2002041,
	NT2RP2002046,	NT2RP2002078,	NT2RP2002124,	NT2RP2002185,	NT2RP2002193,	NT2RP2002312,
	NT2RP2002316,	NT2RP2002426,	NT2RP2002457,	NT2RP2002475,	NT2RP2002520,	NT2RP2002595,
	NT2RP2002643,	NT2RP2002672,	NT2RP2002701,	NT2RP2002710,	NT2RP2002727,	NT2RP2003099,
	NT2RP2003121,	NT2RP2003137,	NT2RP2003158,	NT2RP2003206,	NT2RP2003230,	NT2RP2003272,
20	NT2RP2003280,	NT2RP2003347,	NT2RP2003393,	NT2RP2003401,	NT2RP2003445,	NT2RP2003456,
	NT2RP2003511,	NT2RP2003517,	NT2RP2003543,	NT2RP2003596,	NT2RP2003706,	NT2RP2003871,
	NT2RP2004681,	NT2RP2004743,	NT2RP2004775,	NT2RP2004933,	NT2RP2004967,	NT2RP2005003,
	NT2RP2005270,	NT2RP2005289,	NT2RP2005344,	NT2RP2005453,	NT2RP2005555,	NT2RP2005767,
	NT2RP2005853,	NT2RP2006043,	NT2RP2006393,	NT2RP2006436,	NT2RP2006441,	NT2RP2006467,
25	NT2RP2006534,	NT2RP2006565,	NT2RP3000348,	NT2RP3000359,	NT2RP3000366,	NT2RP3000403,
	NT2RP3000418,	NT2RP3000441,	NT2RP3000561,	NT2RP3000759,	NT2RP3000826,	NT2RP3001007,
	NT2RP3001096,	NT2RP3001126,	NT2RP3001355,	NT2RP3001396,	NT2RP3001449,	NT2RP3001490,
	NT2RP3001679,	NT2RP3001727,	NT2RP3001752,	NT2RP3001777,	NT2RP3001782,	NT2RP3001799,
	NT2RP3001854,	NT2RP3001989,	NT2RP3002142,	NT2RP3002248,	NT2RP3002343,	NT2RP3002484,
30	NT2RP3002529,	NT2RP3002549,	NT2RP3002628,	NT2RP3002687,	NT2RP3002688,	NT2RP3002810,
	NT2RP3003032,	NT2RP3003139,	NT2RP3003193,	NT2RP3003203,	NT2RP3003204,	NT2RP3003210,
	NT2RP3003212,	NT2RP3003264,	NT2RP3003282,	NT2RP3003500,	NT2RP3004041,	NT2RP3004215,
	NT2RP4000147,	NT2RP4000259,	NT2RP4000360,	NT2RP4000448,	NT2RP4000524,	NT2RP4000588,
	NT2RP4000879,	NT2RP4000907,	NT2RP4000989,	NT2RP4001079,	NT2RP4001150,	NT2RP4001219,
35	NT2RP4001260,	NT2RP4001274,	NT2RP4001353,	NT2RP4001547,	NT2RP4001677,	NT2RP4002052,
	OVARC1000006,	OVARC1000092,	OVARC1000321,	OVARC1000384,	OVARC1000408,	OVARC1000414,
	OVARC1000520,	OVARC1000526,	OVARC1000588,	OVARC1000679,	OVARC1000682,	OVARC1000769,
	OVARC1000850,	OVARC1000862,	OVARC1000886,	OVARC1000984,	OVARC1001000,	OVARC1001004,
	OVARC1001154,	OVARC1001170,	OVARC1001173,	OVARC1001200,	OVARC1001268,	OVARC1001376,
40	OVARC1001419,	OVARC1001425,	OVARC1001476,	OVARC1001480,	OVARC1001542,	OVARC1001873,
	OVARC1001928,	OVARC1001987,	OVARC1002066,	OVARC1002082,	OVARC1002112,	OVARC1002127,
	PLACE1000014,	PLACE1000048,	PLACE1000184,	PLACE1000185,	PLACE1000246,	PLACE1000292,
	PLACE1000332,	PLACE1000347,	PLACE1000564,	PLACE1000656,	PLACE1000712,	PLACE1001000,
	PLACE1001168,	PLACE1001185,	PLACE1001241,	PLACE1001294,	PLACE1001311,	PLACE1001395,
45	PLACE1001570,	PLACE1001608,	PLACE1001610,	PLACE1001716,	PLACE1001746,	PLACE1001817,
	PLACE1001821,	PLACE1001844,	PLACE1001897,	PLACE1002066,	PLACE1002119,	PLACE1002157,
	PLACE1002205,	PLACE1002256,	PLACE1002259,	PLACE1002399,	PLACE1002438,	PLACE1002474,
	PLACE1002477,	PLACE1002500,	PLACE1002514,	PLACE1002578,	PLACE1002815,	PLACE1002851,
	PLACE1002968,	PLACE1003108,	PLACE1003174,	PLACE1003200,	PLACE1003238,	PLACE1003256,
50	PLACE1003334,	PLACE1003342,	PLACE1003516,	PLACE1003521,	PLACE1003537,	PLACE1003592,
	PLACE1003596,	PLACE1003723,	PLACE1003760,	PLACE1003771,	PLACE1003783,	PLACE1003795,
	PLACE1003892,	PLACE1003968,	PLACE1004103,	PLACE1004256,	PLACE1004405,	PLACE1004460,
	PLACE1004506,	PLACE1004629,	PLACE1004674,	PLACE1004813,	PLACE1004979,	PLACE1005066,
	PLACE1005101,	PLACE1005102,	PLACE1005128,	PLACE1005181,	PLACE1005287,	PLACE1005305,
55	PLACE1005327,	PLACE1005477,	PLACE1005595,	PLACE1005603,	PLACE1005666,	PLACE1005804,
	PLACE1005884,	PLACE1005934,	PLACE1006076,	PLACE1006119,	PLACE1006159,	PLACE1006164,
	PLACE1006170,	PLACE1006382,	PLACE1006492,	PLACE1006629,	PLACE1006704,	PLACE1006731,
	PLACE1006760,	PLACE1006779,	PLACE1006795,	PLACE1006805,	PLACE1006962,	PLACE1007045,

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	PLACE1007111,	PLACE1007282,	PLACE1007386,	PLACE1007416,	PLACE1007484,	PLACE1007544,
	PLACE1007645,	PLACE1007743,	PLACE1007746,	PLACE1007807,	PLACE1007858,	PLACE1008002,
	PLACE1008181,	PLACE1008273,	PLACE1008368,	PLACE1008405,	PLACE1008532,	PLACE1008568,
	PLACE1008625,	PLACE1008696,	PLACE1008867,	PLACE1009027,	PLACE1009039,	PLACE1009045,
5	PLACE1009110,	PLACE1009298,	PLACE1009328,	PLACE1009581,	PLACE1009621,	PLACE1009622,
	PLACE1009637,	PLACE1009925,	PLACE1009935,	PLACE1010089,	PLACE1010106,	PLACE1010152,
	PLACE1010274,	PLACE1010491,	PLACE1010629,	PLACE1010630,	PLACE1010714,	PLACE1010739,
	PLACE1010891,	PLACE1010896,	PLACE1010925,	PLACE1010965,	PLACE1011026,	PLACE1011046,
	PLACE1011214,	PLACE1011399,	PLACE1011433,	PLACE1011492,	PLACE1011641,	PLACE1011649,
10	PLACE1011719,	PLACE1011762,	PLACE1011858,	PLACE1011923,	PLACE2000014,	PLACE2000039,
	PLACE2000216,	PLACE2000302,	PLACE2000317,	PLACE2000342,	PLACE2000347,	PLACE2000379,
	PLACE3000121,	PLACE3000124,	PLACE3000160,	PLACE3000242,	PLACE3000271,	PLACE3000353,
	PLACE3000362,	PLACE3000365,	PLACE3000400,	PLACE3000401,	PLACE4000034,	PLACE4000089,
	PLACE4000522,	PLACE4000558,				
15	SKNMC1000050,	THYRO1000040,	THYRO1000197,	THYRO1000241,	THYRO1000327,	THYRO1000394,
	THYRO1000488,	THYRO1000501,	THYRO1000585,	THYRO1000596,	THYRO1000625,	THYRO1000805,
	THYRO1000934,	THYRO1001133,	THYRO1001134,	THYRO1001173,	THYRO1001213,	THYRO1001262,
	THYRO1001290,	THYRO1001721,	Y79AA1000037,	Y79AA1000800,	Y79AA1000976,	Y79AA1001078,
	Y79AA1001228,	Y79AA1001299,	Y79AA1001402,	Y79AA1001585,	Y79AA1001696,	Y79AA1001711,
20	Y79AA1001827,	Y79AA1001875,	Y79AA1002027,	Y79AA1002211,	Y79AA1002234,	
	Y79AA1002258,					
	[0226] Clones of which expression levels decrease by RA/inhibitor are as follows:					
	HEMBA1000012,	HEMBA1000501,	HEMBA1000946,	HEMBA1003220,	HEMBA1003403,	HEMBA1003569,
	HEMBA1003591,	HEMBA1003926,	HEMBA1004168,	HEMBA1004507,	HEMBA1005009,	HEMBA1005296,
25	HEMBA1005528,	HEMBA1005570,	HEMBA1006467,	HEMBA1006486,	HEMBA1006492,	HEMBA1007322,
	HEMBB1000055,	HEMBB1000244,	HEMBB1001665,	MAMMA1000684,	MAMMA1001139,	MAMMA1001743,
	NT2RM1000257,	NT2RM1000318,	NT2RM1000539,	NT2RM1000666,	NT2RM2000092,	NT2RM2000192,
	NT2RM2000371,	NT2RM2000594,	NT2RM4000511,	NT2RM4001140,	NT2RM4001754,	NT2RM4001905,
	NT2RM4001940,	NT2RM4002593,	NT2RP1000086,	NT2RP1000439,	NT2RP1001073,	NT2RP2000098,
30	NT2RP2000965,	NT2RP2001397,	NT2RP2002047,	NT2RP2004226,	NT2RP2004396,	NT2RP2004655,
	NT2RP2005126,	NT2RP2005464,	NT2RP2005712,	NT2RP2005859,	NT2RP2005890,	NT2RP3000980,
	NT2RP3001383,	NT2RP3001621,	NT2RP3002081,	NT2RP3002181,	NT2RP3002244,	NT2RP3002590,
	NT2RP3003059,	NT2RP3004258,	NT2RP3004378,	NT2RP3004527,	NT2RP3004594,	NT2RP4001760,
	NT2RP4001950,	NT2RP4002047,	NT2RP4002408,	NT2RP5003459,	OVARC1000004,	OVARC1000035,
35	OVARC1000431,	OVARC1001051,	OVARC1001129,	OVARC1001176,	OVARC1001261,	OVARC1001342,
	OVARC1001942,	OVARC1001943,	PLACE1002171,	PLACE1002465,	PLACE1003190,	PLACE1003375,
	PLACE1004128,	PLACE1005026,	PLACE1005876,	PLACE1005923,	PLACE1007257,	PLACE1007375,
	PLACE1007507,	PLACE1008941,	PLACE1010624,	PLACE1011090,	PLACE1011219,	THYRO1000270,
	Y79AA1000346,	Y79AA1001541,				
40	[0227] Clones of which expression levels increase in the presence of both RA and RA/inhibitor are as follows:					
	HEMBA1000046,	HEMBA1000307,	HEMBA1000504,	HEMBA1000588,	HEMBA1000682,	HEMBA1000726,
	HEMBA1000943,	HEMBA1001071,	HEMBA1001094,	HEMBA1001122,	HEMBA1001323,	HEMBA1001361,
	HEMBA1001455,	HEMBA1001869,	HEMBA1002084,	HEMBA1002583,	HEMBA1002628,	HEMBA1003096,
	HEMBA1003142,	HEMBA1003276,	HEMBA1003309,	HEMBA1003463,	HEMBA1003597,	HEMBA1003617,
45	HEMBA1003725,	HEMBA1003803,	HEMBA1003879,	HEMBA1003989,	HEMBA1004000,	HEMBA1004015,
	HEMBA1004024,	HEMBA1004049,	HEMBA1004056,	HEMBA1004199,	HEMBA1004248,	HEMBA1004356,
	HEMBA1004666,	HEMBA1004770,	HEMBA1004803,	HEMBA1004923,	HEMBA1004934,	HEMBA1004954,
	HEMBA1005039,	HEMBA1005075,	HEMBA1005113,	HEMBA1005219,	HEMBA1005232,	HEMBA1005251,
	HEMBA1005304,	HEMBA1005367,	HEMBA1005410,	HEMBA1005411,	HEMBA1005548,	HEMBA1005581,
50	HEMBA1005631,	HEMBA1005666,	HEMBA1005780,	HEMBA1006485,	HEMBA1006559,	HEMBA1006579,
	HEMBA1006754,	HEMBB1000059,	HEMBB1000575,	HEMBB1000709,	HEMBB1000848,	HEMBB1000985,
	HEMBB1001117,	HEMBB1001210,	HEMBB1001394,	HEMBB1001668,	HEMBB1001695,	HEMBB1002049,
	HEMBB1002254,	HEMBB1002266,	HEMBB1002371,	HEMBB1002614,	HEMBB1002617,	HEMBB1002697,
	MAMMA1000241,	MAMMA1000424,	MAMMA1000616,	MAMMA1000731,	MAMMA1000824,	MAMMA1001038,
55	MAMMA1001243,	MAMMA1002769,	MAMMA1002871,	MAMMA1002941,		
	NT2RM1000725,	NT2RM1000829,	NT2RM2000504,	NT2RM2000635,	NT2RM2000821,	NT2RM2001582,
	NT2RM2001592,	NT2RM2001632,	NT2RM2001648,	NT2RM2001671,	NT2RM2001695,	NT2RM2001879,
	NT2RM4000290,	NT2RM4000425,	NT2RM4000471,	NT2RM4000531,	NT2RM4000852,	NT2RM4001047,

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NT2RM4001454, NT2RM4001557, NT2RM4001566, NT2RM4001582, NT2RM4001953, NT2RM4002409,
 NT2RM4002558, NT2RM4002594, NT2RP1000259, NT2RP1000418, NT2RP1000574, NT2RP1000782,
 NT2RP1000856, NT2RP1000943, NT2RP1000988, NT2RP1001013, NT2RP1001173, NT2RP1001546,
 5 NT2RP2000091, NT2RP2000208, NT2RP2000274, NT2RP2000329, NT2RP2000369, NT2RP2000634,
 NT2RP2001467, NT2RP2001506, NT2RP2001601, NT2RP2001926, NT2RP2001985, NT2RP2002041,
 NT2RP2002046, NT2RP2002078, NT2RP2002124, NT2RP2002193, NT2RP2002312, NT2RP2002316,
 NT2RP2002426, NT2RP2002457, NT2RP2002475, NT2RP2002520, NT2RP2002595, NT2RP2002672,
 10 NT2RP2002701, NT2RP2003099, NT2RP2003137, NT2RP2003206, NT2RP2003230, NT2RP2003272,
 NT2RP2003280, NT2RP2003393, NT2RP2003445, NT2RP2003456, NT2RP2003596, NT2RP2003871,
 NT2RP2004681, NT2RP2004743, NT2RP2004775, NT2RP2004933, NT2RP2004967, NT2RP2005003,
 NT2RP2005289, NT2RP2005453, NT2RP2005555, NT2RP2005767, NT2RP2005853, NT2RP2006043,
 NT2RP2006393, NT2RP2006436, NT2RP2006441, NT2RP2006467, NT2RP2006565, NT2RP3000359,
 NT2RP3000366, NT2RP3000403, NT2RP3000418, NT2RP3000441, NT2RP3000561, NT2RP3000759,
 15 NT2RP3001007, NT2RP3001126, NT2RP3001355, NT2RP3001396, NT2RP3001449, NT2RP3001490,
 NT2RP3001679, NT2RP3001752, NT2RP3001782, NT2RP3001799, NT2RP3001989, NT2RP3002142,
 NT2RP3002248, NT2RP3002343, NT2RP3002484, NT2RP3002529, NT2RP3002549, NT2RP3002687,
 NT2RP3003032, NT2RP3003139, NT2RP3003193, NT2RP3003204, NT2RP3003210, NT2RP3003212,
 20 NT2RP3003264, NT2RP3003282, NT2RP3003500, NT2RP3004041, NT2RP3004215, NT2RP4000147,
 NT2RP4000259, NT2RP4000360, NT2RP4000448, NT2RP4000524, NT2RP4001079, NT2RP4001150,
 NT2RP4001274, NT2RP4001353, NT2RP4001547, NT2RP4001677, OVARC1000092, OVARC1000321,
 OVARC1000384, OVARC1000408, OVARC1000414, OVARC1000520, OVARC1000526, OVARC1000588,
 OVARC1000679, OVARC1000682, OVARC1000769, OVARC1000862, OVARC1000984, OVARC1001000,
 OVARC1001004, OVARC1001154, OVARC1001170, OVARC1001173, OVARC1001200, OVARC1001268,
 25 OVARC1001376, OVARC1001476, OVARC1001542, OVARC1001873, OVARC1001987, OVARC1002082,
 PLACE1000014, PLACE1000048, PLACE1000184, PLACE1000246, PLACE1000292, PLACE1000332,
 PLACE1000347, PLACE1000712, PLACE1001000, PLACE1001294, PLACE1001311, PLACE1001395,
 PLACE1001570, PLACE1001608, PLACE1001610, PLACE1001746, PLACE1001821, PLACE1001844,
 PLACE1001897, PLACE1002066, PLACE1002119, PLACE1002157, PLACE1002205, PLACE1002256,
 30 PLACE1002259, PLACE1002438, PLACE1002474, PLACE1002477, PLACE1002500, PLACE1002578,
 PLACE1002815, PLACE1002851, PLACE1002968, PLACE1003108, PLACE1003174, PLACE1003200,
 PLACE1003256, PLACE1003334, PLACE1003516, PLACE1003592, PLACE1003723, PLACE1003760,
 PLACE1003771, PLACE1003795, PLACE1003892, PLACE1003968, PLACE1004103, PLACE1004256,
 PLACE1004629, PLACE1004979, PLACE1005102, PLACE1005128, PLACE1005305, PLACE1005477,
 35 PLACE1005666, PLACE1005804, PLACE1005934, PLACE1006076, PLACE1006119, PLACE1006159,
 PLACE1006164, PLACE1006170, PLACE1006492, PLACE1006629, PLACE1006704, PLACE1006760,
 PLACE1006795, PLACE1006962, PLACE1007045, PLACE1007386, PLACE1007416, PLACE1007484,
 PLACE1007544, PLACE1007645, PLACE1007743, PLACE1007807, PLACE1007858, PLACE1008002,
 PLACE1008273, PLACE1008368, PLACE1008532, PLACE1008568, PLACE1008696, PLACE1008867,
 40 PLACE1009027, PLACE1009039, PLACE1009298, PLACE1009328, PLACE1009621, PLACE1009637,
 PLACE1010089, PLACE1010106, PLACE1010152, PLACE1010491, PLACE1010630, PLACE1010739,
 PLACE1010896, PLACE1010925, PLACE1010965, PLACE1011046, PLACE1011214, PLACE1011433,
 PLACE1011719, PLACE1011762, PLACE2000039, PLACE2000216, PLACE2000302, PLACE2000342,
 PLACE2000347, PLACE2000379, PLACE3000121, PLACE3000124, PLACE3000242, PLACE3000271,
 45 PLACE3000362, PLACE3000365, PLACE3000400, PLACE3000401, PLACE4000034, PLACE4000089,
 PLACE4000522, PLACE4000558, THYRO1000197, THYRO1000241, THYRO1000327, THYRO1000394,
 THYRO1000488, THYRO1000585, THYRO1000625, THYRO1000805, THYRO1000934, THYRO1001133,
 THYRO1001173, THYRO1001213, THYRO1001262, THYRO1001290, Y79AA1000800, Y79AA1000976,
 Y79AA1001585, Y79AA1001696, Y79AA1001711, Y79AA1002258.
 50 **[0228]** Clones of which expression levels decrease in the presence of both RA and RA/inhibitor are as follows:
 HEMBA1000946, HEMBA1003569, HEMBA1005570, NT2RM1000666, NT2RM2000092, NT2RM2000594,
 NT2RM4001754, NT2RM4001905, NT2RP2002047, NT2RP3000980, NT2RP3002081, NT2RP3004594,
 NT2RP4001950, NT2RP4002408, OVARC1000431, OVARC1001942, OVARC1001943, PLACE1003190,
 PLACE1005923, PLACE1007257, PLACE1010624, Y79AA1000346.
 55 **[0229]** These are neurological disease-associated clones.

Analysis of rheumatoid arthritis-associated genes

[0230] The onset of rheumatoid arthritis is thought to be involved in the proliferation of synovial cells covering inner surfaces of joint cavity and in inflammatory reaction resulted from the action of cytokines produced by leukocytes infiltrating into the joint synovial tissues (Rheumatism Information Center, <http://www.rheuma-net.or.jp/>). Recent studies have also revealed that tissue necrosis factor (TNF)- α participates in the onset (Current opinion in immunology 1999, 11, 657-662). When the expression of a gene exhibits responsiveness to the action of TNF on synovial cells, the gene is considered to be involved in rheumatoid arthritis.

[0231] A survey was performed for genes of which expression levels are varied in response to TNF- α in the primary cell culture of synovial tissue. The primary cultured cells of the smooth muscle (Cell Applications) were grown to be confluent in a culture dish, and then, human TNF- α (Boehringer-Mannheim) was added at a final concentration of 10 ng/ml thereto. The culture was further continued for 24 hours.

[0232] Total RNA was extracted from the cells by using S.N.A.P.^(TM) Total RNA Isolation kit (Invitrogen). The labeling of probe used for hybridization was carried out by using 10 μ g of the total RNA according to the same methods as described above. The data were obtained in triplicate (n=3). The data of signal value representing gene expression level in the cells in the presence of TNF stimulation were compared with those in the absence of the stimulation. The comparison was performed by statistical treatment of two-sample t-test. Clones with significant difference in the signal distribution were selected under the condition of $p < 0.05$. In this analysis,

clones with the difference can be statistically detected even when the signals were low.

Accordingly, clones with signal value of 40 or less were also assessed for the selection.

Table 352 shows the expression level of each cDNA in synovial cells cultured in the absence or presence of TNF.

[0233] Averaged signal values (M_1 , M_2) and sample variances (s_1^2 , s_2^2) for each gene were calculated in each of the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells to be compared. The t-values were determined according to the following formula: $t = (M_1 - M_2) / s / (1/3 + 1/3)^{1/2}$. When the determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01 in the t-distribution table with 4 degrees of freedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p < 0.05$ or $p < 0.01$, respectively.

The tables also include the information of an increase (+) or decrease (-) in the expression level of a gene in the stimulated cells when the level is compared with that of unstimulated cells.

[0234] Clones of which expression levels are elevated by TNF- α are as follows:

HEMBA1000005,	HEMBA1000012,	HEMBA1000020,	HEMBA1000046,	HEMBA1000076,	HEMBA1000111,
HEMBA1000168,	HEMBA1000185,	HEMBA1000201,	HEMBA1000231,	HEMBA1000243,	HEMBA1000280,
HEMBA1000282,	HEMBA1000304,	HEMBA1000307,	HEMBA1000327,	HEMBA1000356,	HEMBA1000376,
HEMBA1000387,	HEMBA1000390,	HEMBA1000418,	HEMBA1000460,	HEMBA1000491,	HEMBA1000501,
HEMBA1000518,	HEMBA1000519,	HEMBA1000520,	HEMBA1000531,	HEMBA1000534,	HEMBA1000542,
HEMBA1000545,	HEMBA1000591,	HEMBA1000592,	HEMBA1000594,	HEMBA1000636,	HEMBA1000655,
HEMBA1000657,	HEMBA1000673,	HEMBA1000682,	HEMBA1000686,	HEMBA1000722,	HEMBA1000726,
HEMBA1000827,	HEMBA1000870,	HEMBA1000918,	HEMBA1000971,	HEMBA1000974,	HEMBA1000986,
HEMBA1001019,	HEMBA1001043,	HEMBA1001051,	HEMBA1001059,	HEMBA1001060,	HEMBA1001071,
HEMBA1001080,	HEMBA1001109,	HEMBA1001140,	HEMBA1001172,	HEMBA1001196,	HEMBA1001213,
HEMBA1001226,	HEMBA1001281,	HEMBA1001299,	HEMBA1001302,	HEMBA1001303,	HEMBA1001323,
HEMBA1001326,	HEMBA1001327,	HEMBA1001330,	HEMBA1001351,	HEMBA1001407,	HEMBA1001411,
HEMBA1001446,	HEMBA1001454,	HEMBA1001569,	HEMBA1001647,	HEMBA1001714,	HEMBA1001800,
HEMBA1001804,	HEMBA1001809,	HEMBA1001888,	HEMBA1001912,	HEMBA1001921,	HEMBA1001967,
HEMBA1002084,	HEMBA1002161,	HEMBA1002166,	HEMBA1002241,	HEMBA1002337,	HEMBA1002363,
HEMBA1002389,	HEMBA1002458,	HEMBA1002460,	HEMBA1002469,	HEMBA1002538,	HEMBA1002542,
HEMBA1002547,	HEMBA1002609,	HEMBA1002624,	HEMBA1002659,	HEMBA1002750,	HEMBA1002770,
HEMBA1002779,	HEMBA1002810,	HEMBA1002816,	HEMBA1002818,	HEMBA1002850,	HEMBA1002863,
HEMBA1003021,	HEMBA1003033,	HEMBA1003078,	HEMBA1003166,	HEMBA1003202,	HEMBA1003204,
HEMBA1003229,	HEMBA1003235,	HEMBA1003276,	HEMBA1003286,	HEMBA1003296,	HEMBA1003370,
HEMBA1003376,	HEMBA1003403,	HEMBA1003418,	HEMBA1003433,	HEMBA1003447,	HEMBA1003560,
HEMBA1003569,	HEMBA1003571,	HEMBA1003591,	HEMBA1003597,	HEMBA1003598,	HEMBA1003621,
HEMBA1003656,	HEMBA1003662,	HEMBA1003680,	HEMBA1003715,	HEMBA1003725,	HEMBA1003729,
HEMBA1003733,	HEMBA1003742,	HEMBA1003773,	HEMBA1003783,	HEMBA1003950,	HEMBA1004012,
HEMBA1004015,	HEMBA1004048,	HEMBA1004074,	HEMBA1004086,	HEMBA1004111,	HEMBA1004131,
HEMBA1004202,	HEMBA1004203,	HEMBA1004207,	HEMBA1004248,	HEMBA1004274,	HEMBA1004321,
HEMBA1004330,	HEMBA1004356,	HEMBA1004366,	HEMBA1004405,	HEMBA1004408,	HEMBA1004429,
HEMBA1004499,	HEMBA1004507,	HEMBA1004509,	HEMBA1004542,	HEMBA1004596,	HEMBA1004604,

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	HEMBA1004776,	HEMBA1004889,	HEMBA1004934,	HEMBA1004978,	HEMBA1005019,	HEMBA1005047,
	HEMBA1005206,	HEMBA1005219,	HEMBA1005274,	HEMBA1005331,	HEMBA1005338,	HEMBA1005394,
	HEMBA1005423,	HEMBA1005576,	HEMBA1005732,	HEMBA1005746,	HEMBA1006091,	HEMBA1006142,
5	HEMBA1006173,	HEMBA1006198,	HEMBA1006253,	HEMBA1006268,	HEMBA1006309,	HEMBA1006377,
	HEMBA1006474,	HEMBA1006486,	HEMBA1006492,	HEMBA1006502,	HEMBA1006535,	HEMBA1006579,
	HEMBA1006648,	HEMBA1006659,	HEMBA1006885,	HEMBA1006929,	HEMBA1006941,	HEMBA1007078,
	HEMBA1007080,	HEMBA1007121,	HEMBA1007194,	HEMBA1007300,	HEMBA1007301,	HEMBA1007322,
	HEMBB1000036,	HEMBB1000044,	HEMBB1000089,	HEMBB1000215,	HEMBB1000217,	HEMBB1000272,
	HEMBB1000420,	HEMBB1000591,	HEMBB1000593,	HEMBB1000631,	HEMBB1000835,	HEMBB1000887,
10	HEMBB1000908,	HEMBB1000975,	HEMBB1000985,	HEMBB1001011,	HEMBB1001014,	HEMBB1001112,
	HEMBB1001133,	HEMBB1001331,	HEMBB1001337,	HEMBB1001366,	HEMBB1001367,	HEMBB1001384,
	HEMBB1001394,	HEMBB1001429,	HEMBB1001463,	HEMBB1001619,	HEMBB1001684,	HEMBB1001706,
	HEMBB1001753,	HEMBB1001797,	HEMBB1001802,	HEMBB1001812,	HEMBB1001874,	HEMBB1001910,
	HEMBB1001915,	HEMBB1001973,	HEMBB1001983,	HEMBB1001990,	HEMBB1002190,	HEMBB1002193,
15	HEMBB1002249,	HEMBB1002329,	HEMBB1002342,	HEMBB1002371,	HEMBB1002409,	HEMBB1002442,
	HEMBB1002489,	HEMBB1002492,	HEMBB1002520,	HEMBB1002534,	HEMBB1002596,	HEMBB1002664,
	HEMBB1002692,	HEMBB1002697,	HEMBB1002705,	MAMMA1000092,	MAMMA1000155,	MAMMA1000163,
	MAMMA1000173,	MAMMA1000175,	MAMMA1000227,	MAMMA1000241,	MAMMA1000257,	MAMMA1000264,
	MAMMA1000266,	MAMMA1000270,	MAMMA1000307,	MAMMA1000410,	MAMMA1000413,	MAMMA1000416,
20	MAMMA1000421,	MAMMA1000472,	MAMMA1000501,	MAMMA1000605,	MAMMA1000643,	MAMMA1000670,
	MAMMA1000684,	MAMMA1000696,	MAMMA1000732,	MAMMA1000752,	MAMMA1000802,	MAMMA1000824,
	MAMMA1000905,	MAMMA1000921,	MAMMA1000931,	MAMMA1000957,	MAMMA1000962,	MAMMA1000998,
	MAMMA1001008,	MAMMA1001050,	MAMMA1001074,	MAMMA1001078,	MAMMA1001292,	MAMMA1001397,
	MAMMA1001476,	MAMMA1001743,	MAMMA1001744,	MAMMA1001754,	MAMMA1001760,	MAMMA1001785,
25	MAMMA1001858,	MAMMA1001908,	MAMMA1002236,	MAMMA1002267,	MAMMA1002292,	MAMMA1002311,
	MAMMA1002322,	MAMMA1002359,	MAMMA1002362,	MAMMA1002485,	MAMMA1002494,	MAMMA1002597,
	MAMMA1002598,	MAMMA1002665,	MAMMA1002671,	MAMMA1002684,	MAMMA1002748,	MAMMA1002775,
	MAMMA1002830,	MAMMA1002858,	MAMMA1002868,	MAMMA1002886,	MAMMA1002887,	MAMMA1002892,
	MAMMA1002909,	MAMMA1002937,	MAMMA1002947,	MAMMA1002964,	MAMMA1002970,	MAMMA1003013,
30	MAMMA1003150,	NT2RM1000039,	NT2RM1000062,	NT2RM1000080,	NT2RM1000086,	NT2RM1000127,
	NT2RM1000132,	NT2RM1000187,	NT2RM1000199,	NT2RM1000244,	NT2RM1000256,	NT2RM1000272,
	NT2RM1000318,	NT2RM1000354,	NT2RM1000377,	NT2RM1000430,	NT2RM1000499,	NT2RM1000539,
	NT2RM1000553,	NT2RM1000563,	NT2RM1000699,	NT2RM1000742,	NT2RM1000826,	NT2RM1000829,
	NT2RM1000833,	NT2RM1000882,	NT2RM1000898,	NT2RM1000905,	NT2RM1001092,	NT2RM2000013,
35	NT2RM2000032,	NT2RM2000042,	NT2RM2000101,	NT2RM2000124,	NT2RM2000192,	NT2RM2000259,
	NT2RM2000260,	NT2RM2000363,	NT2RM2000368,	NT2RM2000402,	NT2RM2000452,	NT2RM2000952,
	NT2RM2001221,	NT2RM2002014,	NT2RM2002030,	NT2RM4000156,	NT2RM4000349,	NT2RM4000395,
	NT2RM4000457,	NT2RM4000511,	NT2RM4000514,	NT2RM4000698,	NT2RM4000764,	NT2RM4001016,
	NT2RM4001084,	NT2RM4001594,	NT2RM4001629,	NT2RM4001662,	NT2RM4001841,	NT2RM4002093,
40	NT2RM4002109,	NT2RM4002145,	NT2RM4002189,	NT2RM4002194,	NT2RM4002226,	NT2RP1000170,
	NT2RP1000439,	NT2RP1000478,	NT2RP1000513,	NT2RP1000701,	NT2RP1000856,	NT2RP1001361,
	NT2RP2000097,	NT2RP2000239,	NT2RP2000288,	NT2RP2000328,	NT2RP2000329,	NT2RP2000369,
	NT2RP2000422,	NT2RP2000842,	NT2RP2000965,	NT2RP2001245,	NT2RP2001440,	NT2RP2001560,
	NT2RP2001634,	NT2RP2001663,	NT2RP2001677,	NT2RP2001762,	NT2RP2002270,	NT2RP2002312,
45	NT2RP2002316,	NT2RP2002333,	NT2RP2002706,	NT2RP2002925,	NT2RP2002959,	NT2RP2002987,
	NT2RP2003125,	NT2RP2003137,	NT2RP2003237,	NT2RP2003272,	NT2RP2003596,	NT2RP2003604,
	NT2RP2003643,	NT2RP2003968,	NT2RP2003976,	NT2RP2004194,	NT2RP2004321,	NT2RP2005037,
	NT2RP2005140,	NT2RP2005204,	NT2RP2005293,	NT2RP2005457,	NT2RP2005555,	NT2RP2005600,
	NT2RP2005701,	NT2RP2005719,	NT2RP2005722,	NT2RP2005773,	NT2RP2005890,	NT2RP2006023,
50	NT2RP2006071,	NT2RP3000186,	NT2RP3000341,	NT2RP3000599,	NT2RP3000632,	NT2RP3000644,
	NT2RP3000852,	NT2RP3000968,	NT2RP3001096,	NT2RP3001109,	NT2RP3001126,	NT2RP3001147,
	NT2RP3001449,	NT2RP3001529,	NT2RP3001753,	NT2RP3001854,	NT2RP3001915,	NT2RP3001969,
	NT2RP3002081,	NT2RP3002142,	NT2RP3002399,	NT2RP3002590,	NT2RP3002603,	NT2RP3002810,
	NT2RP3002876,	NT2RP3003311,	NT2RP3003330,	NT2RP3003672,	NT2RP3004209,	NT2RP3004378,
55	NT2RP4000078,	NT2RP4000541,	NT2RP4000588,	NT2RP4001219,	NT2RP4001228,	NT2RP4001276,
	NT2RP4001507,	NT2RP4002047,	NT2RP5003459,	NT2RP5003492,	OVARC1000085,	OVARC1000087,
	OVARC1000106,	OVARC1000151,	OVARC1000198,	OVARC1000431,	OVARC1000440,	OVARC1000564,
	OVARC1000605,	OVARC1000679,	OVARC1000883,	OVARC1000912,	OVARC1000960,	OVARC1000971,

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OVARC1001038, OVARC1001055, OVARC1001085, OVARC1001129, OVARC1001167, OVARC1001339,
 OVARC1001425, OVARC1001745, OVARC1001762, OVARC1001766, OVARC1001942, OVARC1002044,
 OVARC1002138, PLACE1000004, PLACE1000005, PLACE1000420, PLACE1000547, PLACE1000562,
 PLACE1000653, PLACE1001168, PLACE1001311, PLACE1001377, PLACE1001920, PLACE1001983,
 5 PLACE1002066, PLACE1002072, PLACE1002140, PLACE1002171, PLACE1002319, PLACE1002474,
 PLACE1002499, PLACE1002532, PLACE1002665, PLACE1003025, PLACE1003145, PLACE1003361,
 PLACE1003605, PLACE1003704, PLACE1003783, PLACE1003885, PLACE1004405, PLACE1004629,
 PLACE1004686, PLACE1004930, PLACE1005066, PLACE1006077, PLACE1005630, PLACE1005876,
 PLACE1006143, PLACE1006325, PLACE1006488, PLACE1006805, PLACE1006829, PLACE1007286,
 10 PLACE1007858, PLACE1008201, PLACE1009045, PLACE1009113, PLACE1009621, PLACE1010106,
 PLACE1010310, PLACE1010622, PLACE1010944, PLACE1010965, PLACE1011185, PLACE1011332,
 PLACE1011635, PLACE1011646, PLACE1011725, PLACE2000014, PLACE2000264, PLACE2000394,
 PLACE2000419, PLACE3000160, PLACE3000220, PLACE3000254, PLACE3000271, PLACE3000339,
 PLACE3000341, PLACE3000350, PLACE3000353, PLACE3000401, PLACE4000300, SKNMC1000091,
 15 THYRO1000855, THYRO1001559, Y79AA1000065, Y79AA1000202, Y79AA1000214, Y79AA1000346,
 Y79AA1000784, Y79AA1000833, Y79AA1000968, Y79AA1001555, Y79AA1002220.

[0235] Clones of which expression levels decrease by TNF- α are as follows:

HEMBA1002150, HEMBB1000240, NT2RM2000469, NT2RM2000984, NT2RM2001688, _ NT2RM4000290,
 NT2RM4000496, NT2RM4000590, NT2RM4001047, NT2RM4001582, NT2RM4001611, NT2RM4001650,
 20 NT2RM4002075, NT2RM4002128, NT2RP1000174, NT2RP1000243, NT2RP1000581, NT2RP1000688,
 NT2RP1000767, NT2RP1000825, NT2RP1001185, NT2RP1001286, NT2RP1001432, NT2RP1001457,
 NT2RP2000001, NT2RP2000248, NT2RP2000841, NT2RP2001813, NT2RP2002137, NT2RP2002928,
 NT2RP2003517, NT2RP2003559, NT2RP2003564, NT2RP2004933, NT2RP2005038, NT2RP2006365,
 25 NT2RP3000072, NT2RP3000320, NT2RP3000484, NT2RP3000980, NT2RP3001111, NT2RP3001420,
 NT2RP3001495, NT2RP3002056, NT2RP3002057, NT2RP3002545, NT2RP3002713, NT2RP3002799,
 NT2RP3002869, NT2RP3002953, NT2RP3002955, NT2RP3003282, NT2RP3003290, NT2RP3003384,
 NT2RP3003385, NT2RP3003870, NT2RP3004207, NT2RP3004262, NT2RP3004527, NT2RP4000500,
 NT2RP4000524, NT2RP4000787, NT2RP4000927, NT2RP4000955, NT2RP4000989, NT2RP4001442,
 30 NT2RP4001638, NT2RP4001950, NT2RP4002888, NT2RP5003524, OVARC1001270, PLACE1000246,
 PLACE1002816.

[0236] These are rheumatoid arthritis-associated clones.

Analysis of ultraviolet radiation damage-associated genes

35 **[0237]** It is known that ultraviolet rays give considerably adverse influence on the health. In recent years, there have
 been significant risks of tissue damage by ultraviolet rays because of destruction of the ozone layer. Thus, ultraviolet
 radiation has been recognized as a risk factor for skin diseases such as skin cancers (United States Environmental
 Protection Agency: Ozone Depletion Home Page, <http://www.epa.gov/ozone/>). Genes of which expression levels are
 40 varied in skin epidermal cells exposed to ultraviolet rays are considered to be associated with skin damage caused by
 ultraviolet radiation.

[0238] After primary cultured skin fibroblast cells were irradiated with ultraviolet ray and were cultured, a survey was
 performed for genes of which expression levels were varied depending on the irradiation of ultraviolet ray. First, after
 cultured to be confluent, the primary cultured skin fibroblast cells (Cell Applications) were exposed to 10,000 $\mu\text{J}/\text{cm}^2$
 of 254-nm ultraviolet light.

45 **[0239]** Messenger RNAs were, then, extracted by using a FastTrack™ 2.0 mRNA Isolation kit (Invitrogen Co.) from
 the unexposed cells and from the cells that were exposed to the ultraviolet light and then cultured for 4 or 24 hours.
 The labeling of the hybridization probe was carried out by using a 1.5 μg of each mRNA in the same manner as
 described above. The data were obtained in triplicate ($n=3$). The hybridization signals were compared between the
 cells exposed to the ultraviolet light and the unexposed cells. The comparison was performed by statistical treatment
 50 with two-sample t-test. Clones with significant differences in the signal distribution were selected under the condition
 of $p<0.05$. In this analysis, even when the signal is lower than others, the difference in the signal values can be detected
 statistically. Accordingly, clones with signal value of 40 or lower were also assessed for selection.

[0240] Tables 353-509 show the expression of each cDNA in skin-derived fibroblast cells exposed and unexposed
 to ultraviolet light.

55 **[0241]** Averaged signal values (M_1 , M_2) and sample variances (s_1^2 , s_2^2) were calculated for each gene in each of
 the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells
 to be compared. The t values were determined according to the following formula: $t=(M_1-M_2)/s/(1/3+1/3)^{1/2}$. When the
 determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01

in the t-distribution table with 4 degrees of freedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p < 0.05$ or $p < 0.01$, respectively. The tables also include the information of an increase (+) or decrease (-) in the expression level of a gene in the exposed cells in comparison with that of unexposed cells.

- 5 **[0242]** The expression levels of the following clones were elevated 4 or 24 hours after the ultraviolet irradiation:
 HEMBA1000542, HEMBA1001808, HEMBA1002177, HEMBA1003314, MAMMA1001874, NT2RM2001100,
 NT2RP2005732, NT2RP3000592, NT2RP4000657, OVARC1000004, OVARC1001092, OVARC1001342,
 PLACE1002816, NT2RM4001002, NT2RM4001813, NT2RM4002266, NT2RP2001174, NT2RP2001196,
 NT2RP2005358, NT2RP3000690, NT2RP3001216, NT2RP3003464, PLACE1006382, THYRO1000070,
 10 THYRO1001100, Y79AA1000342.
- [0243]** The expression levels of the following clones were decreased 4 or 24 hours after the ultraviolet irradiation:
 HEMBA1000005, HEMBA1000150, HEMBA1000156, HEMBA1000158, HEMBA1000168, HEMBA1000231,
 HEMBA1000304, HEMBA1000307, HEMBA1000333, HEMBA1000366, HEMBA1000369, HEMBA1000390,
 HEMBA1000396, HEMBA1000418, HEMBA1000434, HEMBA1000464, HEMBA1000469, HEMBA1000490,
 15 HEMBA1000504, HEMBA1000505, HEMBA1000557, HEMBA1000657, HEMBA1000673, HEMBA1000682,
 HEMBA1000686, HEMBA1000727, HEMBA1000752, HEMBA1000851, HEMBA1000852, HEMBA1000870,
 HEMBA1000872, HEMBA1001085, HEMBA1001121, HEMBA1001133, HEMBA1001235, HEMBA1001265,
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	PLACE1000347,	PLACE1000374,	PLACE1000424,	PLACE1000492,	PLACE1000547,	PLACE1000564,
	PLACE1000599,	PLACE1000653,	PLACE1000706,	PLACE1000748,	PLACE1000749,	PLACE1000755,
	PLACE1000841,	PLACE1000849,	PLACE1000856,	PLACE1000931,	PLACE1000987,	PLACE1001015,
	PLACE1001024,	PLACE1001054,	PLACE1001062,	PLACE1001118,	PLACE1001168,	PLACE1001238,
30	PLACE1001377,	PLACE1001383,	PLACE1001384,	PLACE1001399,	PLACE1001440,	PLACE1001503,
	PLACE1001545,	PLACE1001611,	PLACE1001640,	PLACE1001691,	PLACE1001705,	PLACE1001740,
	PLACE1001817,	PLACE1001844,	PLACE1001845,	PLACE1001869,	PLACE1001897,	PLACE1002004,
	PLACE1002073,	PLACE1002140,	PLACE1002157,	PLACE1002171,	PLACE1002205,	PLACE1002213,
	PLACE1002474,	PLACE1002500,	PLACE1002529,	PLACE1002537,	PLACE1002598,	PLACE1002655,
35	PLACE1002908,	PLACE1003045,	PLACE1003136,	PLACE1003174,	PLACE1003258,	PLACE1003296,
	PLACE1003334,	PLACE1003342,	PLACE1003361,	PLACE1003366,	PLACE1003369,	PLACE1003420,
	PLACE1003454,	PLACE1003553,	PLACE1003566,	PLACE1003583,	PLACE1003669,	PLACE1003711,
	PLACE1003723,	PLACE1003738,	PLACE1003760,	PLACE1003762,	PLACE1003771,	PLACE1003783,
	PLACE1003850,	PLACE1003858,	PLACE1003915,	PLACE1004128,	PLACE1004161,	PLACE1004183,
40	PLACE1004197,	PLACE1004302,	PLACE1004358,	PLACE1004437,	PLACE1004460,	PLACE1004471,
	PLACE1004506,	PLACE1004518,	PLACE1004646,	PLACE1004722,	PLACE1004793,	PLACE1004804,
	PLACE1004838,	PLACE1004868,	PLACE1004900,	PLACE1004902,	PLACE1004969,	PLACE1004979,
	PLACE1005086,	PLACE1005162,	PLACE1005243,	PLACE1005266,	PLACE1005313,	PLACE1005584,
	PLACE1005698,	PLACE1005727,	PLACE1005739,	PLACE1005851,	PLACE1005925,	PLACE1006196,
45	PLACE1006248,	PLACE1006262,	PLACE1006335,	PLACE1006360,	PLACE1006385,	PLACE1006412,
	PLACE1006414,	PLACE1006445,	PLACE1006598,	PLACE1006629,	PLACE1006640,	PLACE1006792,
	PLACE1006815,	PLACE1006901,	PLACE1006917,	PLACE1006962,	PLACE1007021,	PLACE1007045,
	PLACE1007112,	PLACE1007226,	PLACE1007243,	PLACE1007454,	PLACE1007547,	PLACE1007598,
	PLACE1007618,	PLACE1007645,	PLACE1007649,	PLACE1007706,	PLACE1007725,	PLACE1007746,
50	PLACE1007843,	PLACE1007877,	PLACE1007954,	PLACE1007969,	PLACE1008002,	PLACE1008095,
	PLACE1008111,	PLACE1008132,	PLACE1008273,	PLACE1008275,	PLACE1008331,	PLACE1008356,
	PLACE1008368,	PLACE1008402,	PLACE1008603,	PLACE1008650,	PLACE1008696,	PLACE1008757,
	PLACE1008807,	PLACE1008867,	PLACE1008941,	PLACE1009020,	PLACE1009039,	PLACE1009158,
	PLACE1009172,	PLACE1009190,	PLACE1009230,	PLACE1009319,	PLACE1009338,	PLACE1009375,
55	PLACE1009434,	PLACE1009613,	PLACE1009637,	PLACE1009659,	PLACE1009763,	PLACE1009845,
	PLACE1009921,	PLACE1009971,	PLACE1009992,	PLACE1010023,	PLACE1010053,	PLACE1010069,
	PLACE1010074,	PLACE1010181,	PLACE1010202,	PLACE1010231,	PLACE1010270,	PLACE1010274,
	PLACE1010321,	PLACE1010329,	PLACE1010492,	PLACE1010522,	PLACE1010616,	PLACE1010624,

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	PLACE1010631,	PLACE1010786,	PLACE1011032,	PLACE1011114,	PLACE1011221,	PLACE1011325,
	PLACE1011520,	PLACE1011635,	PLACE1011649,	PLACE1011682,	PLACE1011875,	PLACE1011896,
	PLACE1011964,	PLACE1012031,	PLACE2000015,	PLACE2000021,	PLACE2000047,	PLACE2000072,
5	PLACE2000097,	PLACE2000136,	PLACE2000246,	PLACE2000302,	PLACE2000379,	PLACE2000394,
	PLACE2000425,	PLACE2000427,	PLACE2000477,	PLACE3000009,	PLACE3000070,	PLACE3000142,
	PLACE3000145,	PLACE3000148,	PLACE3000155,	PLACE3000169,	PLACE3000208,	PLACE3000230,
	PLACE3000322,	PLACE3000331,	PLACE3000352,	PLACE3000401,	PLACE3000413,	PLACE3000425,
	PLACE3000477,	PLACE4000009,	PLACE4000049,	PLACE4000089,	PLACE4000100,	PLACE4000247,
	PLACE4000250,	PLACE4000252,	PLACE4000300,	PLACE4000344,	PLACE4000367,	PLACE4000465,
10	PLACE4000489,	PLACE4000638,	SKNMC1000013,	THYRO1000017,	THYRO1000026,	THYRO1000034,
	THYRO1000072,	THYRO1000132,	THYRO1000173,	THYRO1000190,	THYRO1000197,	THYRO1000221,
	THYRO1000253,	THYRO1000270,	THYRO1000279,	THYRO1000327,	THYRO1000394,	THYRO1000438,
	THYRO1000558,	THYRO1000569,	THYRO1000585,	THYRO1000596,	THYRO1000625,	THYRO1000637,
	THYRO1000676,	THYRO1000734,	THYRO1000777,	THYRO1000783,	THYRO1000805,	THYRO1000843,
15	THYRO1000934,	THYRO1001033,	THYRO1001347,	THYRO1001405,	THYRO1001411,	THYRO1001534,
	THYRO1001573,	THYRO1001584,	THYRO1001602,	THYRO1001605,	THYRO1001772,	THYRO1001854,
	VESEN1000122,	Y79AA1000037,	Y79AA1000065,	Y79AA1000181,	Y79AA1000231,	Y79AA1000349,
	Y79AA1000355,	Y79AA1000368,	Y79AA1000538,	Y79AA1000782,	Y79AA1001023,	Y79AA1001145,
	Y79AA1001391,	Y79AA1001541,	Y79AA1001585,	Y79AA1001705,	Y79AA1001781,	Y79AA1001923,
20	Y79AA1001963,	Y79AA1002125,	Y79AA1002229,	Y79AA1002407,	Y79AA1002487,	

[0244] These clones are ultraviolet radiation damage-associated clones.

Table 12

Expression of each cDNA in human tissues (containing clones that are not described in Examples.)

Table 349

5	Y79AA1002361	5.46	3.35	2.57	6.5	7.83	6.14	2.75	4.60	4.6	*	+		
	Y79AA1002365	1.93	1.66	1.86	2.93	2.21	2.54	1.34	2.05	2.05	*	+		
	Y79AA1002373	3.38	1.43	1.37	3.37	3.29	2.38	2.95	2.21	2.21				
	Y79AA1002376	434.81	300.04	466.40	120.28	171.61	120.00	316.81	454.58	454.6	**	-		
	Y79AA1002378	5.45	6.92	5.32	7.99	10.13	8.03	4.87	4.92	4.92	*	+		
10	Y79AA1002381	11.63	11.08	9.56	16.28	16.98	14.53	7.89	7.01	7.01	**	+	**	-
	Y79AA1002388	4.34	4.47	7.01	11.41	12.79	9.45	5.70	6.37	6.37	*	+		
	Y79AA1002399	4.43	1.48	1.47	4.2	2.82	2.25	3.39	3.35	3.35				
	Y79AA1002407	1.81	1.09	1.32	2.36	2.58	2.43	1.55	2.35	2.35	**	+		
	Y79AA1002413	15.88	6.76	10.60	19.95	26.46	17.33	9.58	12.56	12.56				
15	Y79AA1002416	5.12	2.89	2.97	4.45	4.32	5.10	4.13	4.19	4.19				
	Y79AA1002429	2.82	1.17	1.77	2.75	1.85	2.91	4.10	5.62	5.62			*	+
	Y79AA1002431	4.04	2.82	3.86	2.55	4.38	4.86	4.06	5.56	5.56	-			
	Y79AA1002433	11.76	5.78	6.28	9.49	4.53	7.78	4.34	8.17	8.17				
20	Y79AA1002445	10.95	9.11	9.11	11.15	8.78	14.80	10.37	11.14	11.14				
	Y79AA1002461	10.04	5.58	4.92	9.55	8.99	8.05	5.89	7.75	7.75				
	Y79AA1002466	22.18	13.94	11.33	23.59	18.02	25.25	10.79	17.76	17.76				
	Y79AA1002471	5.76	3.00	5.65	6.94	8.49	9.26	5.31	7.89	7.89	*	+		
	Y79AA1002472	12.12	5.83	9.20	16.86	14.60	20.34	6.74	12.38	12.38	*	+		
25	Y79AA1002474	3.46	0.84	1.92	1.74	1.49	1.64	2.77	1.35	1.35				
	Y79AA1002482	13.92	8.55	11.10	23.82	23.90	29.62	10.40	14.99	14.99	**	+		
	Y79AA1002487	1.72	0.87	1.11	1.3	1.59	1.75	1.57	1.93	1.93				
	Y79AA1002490	13.58	4.80	6.45	5.13	6.72	3.78	4.31	7.19	7.19				
	Y79AA1002493	5.77	2.96	3.11	8.04	10.37	7.90	4.77	5.75	5.75	*	+		
30	ZRV6C1006278	1.43	0.95	1.01	1.16	2.05	0.47	1.35	2.06	2.06				

[0245] The correspondence of the full-length nucleotide sequences of the present invention and the corresponding deduced amino acid sequences with the clone names are shown below.

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	NT2RP4000724	C-NT2RP4000724	12135	12136
	NT2RP4000728	C-NT2RP4000728	12137	12138
5	NT2RP4000737	C-NT2RP4000737	12139	12140
	NT2RP4000739	C-NT2RP4000739	12141	12142
	NT2RP4000781	C-NT2RP4000781	12143	12144
10	NT2RP4000817	C-NT2RP4000817	12145	12146
	NT2RP4000833	C-NT2RP4000833	12147	12148
	NT2RP4000837	C-NT2RP4000837	12149	12150
	NT2RP4000839	C-NT2RP4000839	12151	12152
15	NT2RP4000855	C-NT2RP4000855	12153	12154
	NT2RP4000865	C-NT2RP4000865	12155	12156
	NT2RP4000878	C-NT2RP4000878	12157	12158
	NT2RP4000879	C-NT2RP4000879	12159	12160
20	NT2RP4000925	C-NT2RP4000925	12161	12162
	NT2RP4000927	C-NT2RP4000927	12163	12164
	NT2RP4000928	C-NT2RP4000928	12165	12166
25	NT2RP4000929	C-NT2RP4000929	12167	12168
	NT2RP4000955	C-NT2RP4000955	12169	12170
	NT2RP4000973	C-NT2RP4000973	12171	12172
	NT2RP4000975	C-NT2RP4000975	12173	12174
30	NT2RP4000979	C-NT2RP4000979	12175	12176
	NT2RP4000984	C-NT2RP4000984	12177	12178
	NT2RP4000989	C-NT2RP4000989	12179	12180
	NT2RP4000997	C-NT2RP4000997	12181	12182
35	NT2RP4001004	C-NT2RP4001004	12183	12184
	NT2RP4001006	C-NT2RP4001006	12185	12186
	NT2RP4001010	C-NT2RP4001010	12187	12188
40	NT2RP4001041	C-NT2RP4001041	12189	12190
	NT2RP4001057	C-NT2RP4001057	12191	12192
	NT2RP4001064	C-NT2RP4001064	12193	12194
	NT2RP4001079	C-NT2RP4001079	12195	12196
45	NT2RP4001080	C-NT2RP4001080	12197	12198
	NT2RP4001086	C-NT2RP4001086	12199	12200
	NT2RP4001095	C-NT2RP4001095	12201	12202
50	NT2RP4001100	C-NT2RP4001100	12203	12204
	NT2RP4001117	C-NT2RP4001117	12205	12206
	NT2RP4001122	C-NT2RP4001122	12207	12208
	NT2RP4001126	C-NT2RP4001126	12209	12210
55	NT2RP4001138	C-NT2RP4001138	12211	12212

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	NT2RP4000996	3.54	3.54	7.49	6.77	6.52	7.38		
	NT2RP4000997	21.59	21.59	36.81	28.52	15.18	34.38		
5	NT2RP4001001	5.53	5.53	9.17	16.66	18.38	15.09	**	+
	NT2RP4001004	1.71	1.71	4.88	2.84	3.09	1.37		
	NT2RP4001006	3.46	3.46	8.12	6.85	6.52	6.13		
10	NT2RP4001009	9.3	9.3	10.45	15.44	20.46	8.25		
	NT2RP4001010	7.33	7.33	9.13	7.38	9.75	6.68		
	NT2RP4001013	23.29	23.29	50.16	30.87	28.1	30.91		
	NT2RP4001029	2.49	2.49	5.95	4.05	2.84	3.63		
15	NT2RP4001036	7.55	7.55	13.55	9.11	11.51	13.16		
	NT2RP4001041	6.57	6.57	14.4	9.89	12.3	6.35		
	NT2RP4001042	4.34	4.34	8.11	9.44	12.5	8.79		
20	NT2RP4001046	6.98	6.98	9.95	13.24	16.28	15.36	**	+
	NT2RP4001050	5.28	5.28	4.81	3.79	4.64	3.35	*	-
	NT2RP4001051	6.48	6.48	8.44	5.43	6.82	5.26		
	NT2RP4001057	0.76	0.76	2.19	2.34	2.43	1.87		
25	NT2RP4001063	1.48	1.48	4.39	3.34	3.53	1.8		
	NT2RP4001064	3.51	3.51	9.18	12.02	9.13	11.57		
	NT2RP4001067	4.42	4.42	9.77	10.96	9.63	6.6		
30	NT2RP4001078	2.12	2.12	3.43	2.67	2.53	1.82		
	NT2RP4001079	5.3	5.3	9.35	8.51	8.02	8.98		
	NT2RP4001080	4.1	4.1	5.27	3.52	4.52	2.3		
	NT2RP4001086	5.08	5.08	4.19	3.93	6.64	2.85		
35	NT2RP4001095	2.49	2.49	7.25	7.96	6.49	6.85		
	NT2RP4001098	0.92	0.92	3.38	3.87	2.95	3.41		
	NT2RP4001100	6.47	6.47	24.34	20.89	20.64	16.99		
	NT2RP4001105	3.13	3.13	7.23	6.51	5.58	4.61		
40	NT2RP4001110	1.75	1.75	3.5	7.07	8.35	5.29	*	+
	NT2RP4001115	9.95	9.95	17.68	20.6	18.48	15.31		
	NT2RP4001117	19.81	19.81	30.49	35.35	42.53	27.5		
45	NT2RP4001122	6.06	6.06	6.09	5.17	6.25	3.27		
	NT2RP4001123	3.62	3.62	7.76	7.95	5.96	6.27		
	NT2RP4001126	4.36	4.36	11.28	10.87	9.09	8.04		
	NT2RP4001127	3.25	3.25	4.59	3.39	3.08	2.17		
50	NT2RP4001138	2.46	2.46	5.8	3.41	2.56	1.62		
	NT2RP4001143	2.73	2.73	5.98	6.44	6.54	5.66		
	NT2RP4001148	3.72	3.72	6.76	3.77	3.03	2.05		
55	NT2RP4001149	5.07	5.07	7.28	6.76	9.03	6.37		
	NT2RP4001150	3.8	3.8	3.17	3.15	3.7	2.88		

Table 353

5 Expression of each cDNA in skin-derived fibroblast cells exposed and unexposed to ultraviolet light (the table also includes clones that are not described in Examples)

10 In the table, UV_0h represents skin-derived fibroblast cells without ultraviolet irradiation; UV_4h and UV_24h represent skin-derived fibroblast cells 4 and 24 hours, respectively, after the irradiation. The assay was performed in triplicate (n=3) and each result is shown in the column of Exp1, Exp2, or Exp3. "t-test 0/4" and "t-test 0/24" represent the results of the test for significant difference between the unexposed cells and the cells 4 hours after the irradiation, and
15 between the unexposed cells and the cells 24 hours after the irradiation, respectively. The table also includes the information on an increase (+) or decrease (-) in the expression level of the gene in the exposed cells 4 hours or 24 hours after the ultraviolet light irradiation. The results of the test for significant difference are shown in the columns of *p<0.05 and **p<0.01.
20

Table 455

	NT2RP4000949	10.71	9.2	16.65	6.86	2.65	3.74	2.78	1.39	2.41	*	*	-	-
	NT2RP4000955	5.81	4.35	6.4	6.28	2.77	1.08	2.31	3.19	3.37	*	*	-	-
5	NT2RP4000959	46.28	46.79	57.49	28.43	49.02	25.11	20.47	30.52	16.93	**	*	-	-
	NT2RP4000962	11.98	9.47	12.39	11.59	10.69	8.83	6.01	4.92	5.77	**	*	-	-
	NT2RP4000973	21.72	16.11	23.28	13.29	14.47	13.18	9.73	13.42	15.34	*	*	-	-
	NT2RP4000975	12.7	11.46	22.76	9.51	5.19	6.19	5.82	10.95	9.25			-	-
	NT2RP4000979	15.15	9.34	21.99	15.27	12.98	9.04	9.28	10.97	8.24			-	-
	NT2RP4000984	6.41	8.08	14.46	6.57	1.97	3.73	2.22	3.31	3.09			-	-
10	NT2RP4000986	6.86	5.41	12.86	6.12	4.31	1.27	1.5	2.5	1.16	*	*	-	-
	NT2RP4000988	17.65	11.88	13.93	10.42	7.43	7.63	9.24	12.28	11.72	*	*	-	-
	NT2RP4000989	4.65	7.43	6.1	6.61	2.52	1.81	2.98	2.09	3.85	*	*	-	-
	NT2RP4000990	6.25	7.92	5.23	9.42	4.63	4.12	5.36	2.51	2.44			-	-
	NT2RP4000994	8.9	9.21	16.92	10.87	4.94	9.69	11.79	23.69	21.99			-	-
	NT2RP4000996	77.3	49.17	79.6	45.61	34.69	39.35	32.71	38.95	46.1	*	*	-	-
15	NT2RP4000997	122.55	129.24	107.05	94.09	70.8	26.94	46.25	80.17	57.14	**	*	-	-
	NT2RP4001001	12.46	18.44	15.8	14.39	8.88	9.17	8.14	8.28	5.33	*	*	-	-
	NT2RP4001004	5.22	3.76	7.06	6.01	1.06	2.64	1.83	1.39	1.05	*	*	-	-
	NT2RP4001006	13.89	13.25	17.25	8.9	7.61	7.07	7.25	6.36	7.3	**	**	-	-
	NT2RP4001009	16.48	20.86	24.07	12.83	13.33	10.38	13	7.19	7.56	*	*	-	-
20	NT2RP4001010	12.07	13.64	9.65	9.47	5.84	7.62	5.8	4.44	3.25	**	*	-	-
	NT2RP4001013	109.49	147.49	90.54	50.6	80.74	63.83	38.95	52.28	51.67	*	*	-	-
	NT2RP4001029	20.54	17.68	29.5	9.58	9.72	9.68	7.27	4.7	8.7	*	*	-	-
	NT2RP4001036	9.27	12.23	13.79	8.52	7.63	4.92	8.03	6.75	4.44	*	*	-	-
	NT2RP4001041	36.4	40.27	32.69	14.35	15.64	11.72	23.48	9.92	16.78	**	*	-	-
	NT2RP4001042	15.67	10.3	17.88	10.18	7.53	8.42	5.86	5.84	7.9	*	*	-	-
	NT2RP4001046	36.69	45.09	54.4	22.18	26.84	16.1	31.95	24.71	14.49	*	*	-	-
25	NT2RP4001050	14.02	22.04	12.83	10.97	2.91	3.84	9.37	3.59	3.94	*	*	-	-
	NT2RP4001051	21.06	26.13	23.41	17.4	11.41	16.25	15.66	11.32	18.06	*	*	-	-
	NT2RP4001057	5.02	3.25	6.98	7.18	2.13	3.82	4.33	2.83	3.14			-	-
	NT2RP4001063	6.13	4.37	7.2	7.29	2.91	4.39	2.87	3.18	3.35	*	*	-	-
	NT2RP4001064	9.3	9.96	15.17	12.02	5.98	5.07	7.19	9.48	7.97			-	-
30	NT2RP4001067	10.58	14.37	13.96	6.93	4.54	4.48	7.26	9.16	8.36	**	*	-	-
	NT2RP4001078	4	5.51	5.6	4.49	1.94	2.06	3.66	2.7	1.04	*	*	-	-
	NT2RP4001079	8.77	14.47	11.97	8.98	3.49	1.98	7.36	2.56	7.44			-	-
	NT2RP4001080	8.56	8.71	5.39	7.24	5.74	5.86	5.43	5.54	6.58			-	-
	NT2RP4001086	8.1	13.85	11.2	8.73	5.59	7.65	7.59	3.27	6.54			-	-
	NT2RP4001095	21.9	10.2	20.98	20.1	8.21	22.42	25.97	28.91	25.72			-	-
35	NT2RP4001098	9.87	7.14	14.73	8.69	4.17	6.42	4.56	7.67	4.16			-	-
	NT2RP4001100	87.64	83.13	87.53	54.87	47.17	71.93	63.14	104.74	100.86	*	*	-	-
	NT2RP4001105	4.62	5.85	6.18	8.6	3.1	3.62	2.72	2.96	3.35	**	*	-	-
	NT2RP4001110	4.35	3.52	3.95	6.4	1.65	2.39	2.86	1.95	2.46	*	*	-	-
	NT2RP4001115	9.9	15.92	16.54	12.73	4.3	5.05	12.1	7.78	11.14			-	-
	NT2RP4001117	47.61	50.63	46.56	30.24	19.2	17.67	37.4	37.77	12.69	**	*	-	-
40	NT2RP4001122	7.49	13.49	11.17	8.93	3.06	4.64	5.55	4.07	4.81	*	*	-	-
	NT2RP4001123	15.99	10.87	15.29	13.96	11.8	8.64	4.92	11.31	11.27			-	-
	NT2RP4001126	32.2	22.75	27.43	23.25	13.48	17.12	8.86	11.87	13.23	**	*	-	-
	NT2RP4001127	5.7	5.54	5.37	7.61	3.72	4.66	3.57	2.2	3.61	**	*	-	-
	NT2RP4001138	6.95	3.88	7.12	9.78	5.56	5.09	4.09	4.44	3.91			-	-
	NT2RP4001143	12.5	11.65	11.43	11.35	7.29	7.76	9.34	8.18	11.45			-	-
45	NT2RP4001148	6.15	6.48	10.09	9.88	3.88	5.87	3.55	2.98	4.94			-	-
	NT2RP4001149	10.56	12.29	14.62	14.76	6.44	4.57	8.21	6.46	7.23	*	*	-	-
	NT2RP4001150	2.08	2.58	2.6	5.53	2.21	2.02	2.86	2.61	5.29			-	-
	NT2RP4001159	28.55	18.66	30.75	17.14	15.33	13.97	7.91	12.94	18.83			-	-
	NT2RP4001162	19.05	7.92	22.71	10.51	6.28	6.36	7.29	6.36	7.28			-	-
	NT2RP4001170	4.82	3.9	7.97	5.23	1.81	3.87	2.53	3.13	2.09			-	-
50	NT2RP4001174	28.66	24.87	30.19	18.62	12.05	22.33	28.65	25.07	34.84	*	*	-	-
	NT2RP4001175	41.57	44.74	48.16	32.54	33.99	41.64	26.8	24.72	38.38	*	*	-	-
	NT2RP4001176	940.52	839.83	1091.9	860.36	609.5	960.82	721.44	858.51	780.83			-	-
	NT2RP4001184	63.86	45.01	63.95	60.3	52	64.4	59.44	58.17	76.19			-	-
	NT2RP4001198	36.14	14.18	33.12	25.99	15.11	24.84	10.23	17.15	15.95			-	-
	NT2RP4001199	7.47	5.66	10.86	10.65	3.07	4.16	4.96	7.07	8.52			-	-
55	NT2RP4001206	64.73	49.7	69.67	51.07	49.14	54.08	37.12	41.91	43.36	*	*	-	-
	NT2RP4001207	7.32	3.58	10.38	7.77	2.4	3.4	3.22	3.79	1.65			-	-
	NT2RP4001210	10.03	7.34	12.93	9.04	5.66	7.56	3.96	6.73	5.83			-	-

Table 509

	Y79AA1002206	7.86	6.79	4.86	2.41	3.6	5.74	5.49	1.51	2.8				
5	Y79AA1002208	21.91	17.64	15.14	5.6	4.07	5.57	6.81	5.17	2.55	**	**	-	-
	Y79AA1002209	14.82	11.28	11.86	6.23	4.7	2.82	4.71	1.33	3.18	**	**	-	-
	Y79AA1002210	13.64	7.39	7.59	9.08	4.62	5.18	20.5	2.05	6.37				
	Y79AA1002211	11.76	19.59	13.47	10.43	6.65	6.52	12.32	8.42	11.25				
	Y79AA1002213	40.78	31.99	22.96	18.41	26.57	14.98	45.88	32.4	41.97				
	Y79AA1002215	54.92	41.69	39.55	24.88	24.36	11.26	37.49	23.6	35.98	*		-	-
10	Y79AA1002220	17.03	11.5	20.58	7.13	5.68	5.31	4.57	4.8	6.51	*	*	-	-
	Y79AA1002226	48.55	31.27	31.34	7.35	12.72	13.65	9.19	6.65	11.13	*	**	-	-
	Y79AA1002229	7.88	6.84	5.37	6.02	4.67	2.85	3.67	2.52	3.73	*	*	-	-
	Y79AA1002234	20.83	13.27	12.39	9.34	6.36	3.6	6.9	3.36	5.84	*	*	-	-
	Y79AA1002235	28.03	23.84	21.24	15.07	14.87	9.39	10.75	8.42	13.64	*	**	-	-
15	Y79AA1002246	9.72	14.9	10.35	5.25	6.99	4.12	8.31	3.82	6.69	*		-	-
	Y79AA1002258	12.35	12.02	7.88	7.82	11.57	8.55	9.77	4.5	4.81				
	Y79AA1002279	51.52	49.19	41.11	5.28	2.78	2.07	15.99	20.03	22.13	**	**	-	-
	Y79AA1002292	13.64	7.58	4.14	5.73	4.43	2.94	6.45	6.01	8.36				
	Y79AA1002298	9.43	8.29	4.77	3.29	5.48	4.2	4.42	4.85	3.79				
20	Y79AA1002307	9.31	8.07	6.62	3.9	4.4	2.44	5.17	1.76	2.58	*	*	-	-
	Y79AA1002309	8.88	7.96	8.79	3.32	4.26	2.83	4.23	2.88	3.97	**	**	-	-
	Y79AA1002311	16.51	9.27	11.76	6.9	6.2	3.45	7.45	3.09	6.4	*		-	-
	Y79AA1002334	13.05	8.36	7.7	5.13	4.89	3.36	5.91	4.32	5.92	*		-	-
	Y79AA1002351	13.61	12.49	9.42	7.1	4.15	6.19	7.95	4.93	5.8	*	*	-	-
	Y79AA1002355	31.74	30.6	21.85	12.21	15.81	9.74	20.54	18.29	18.48	*	*	-	-
25	Y79AA1002361	23.42	15.4	18.02	12.53	10.73	6.85	25.86	17.1	25.5	*		-	-
	Y79AA1002365	12.42	6.37	7.19	3.15	4.11	3.03	4.29	4.74	4.01				
	Y79AA1002373	8.95	6.89	5.46	5.13	4.81	3.4	9.6	4.57	7.84	*		-	-
	Y79AA1002376	1550.5	2569.2	1680.8	462.62	827.86	616.71	1477.6	1040.3	1062.1	*		-	-
	Y79AA1002378	20.24	17.32	13.54	5.14	9.41	4.23	19.28	11.07	16.88	*		-	-
30	Y79AA1002381	116.11	128.86	74.48	110.66	141.78	92.68	155.95	123.08	170.94				
	Y79AA1002388	33.4	33.3	27.31	13.85	26.75	11.62	21.29	16.32	21.24		*	-	-
	Y79AA1002399	11.13	8.22	7.72	4.28	5.54	4.87	7.56	5.9	6.25	*		-	-
	Y79AA1002407	12.66	14.43	18.13	7.72	14.18	6.84	5.83	9.78	4.59	*	*	-	-
	Y79AA1002413	16.98	12.77	14.95	6.14	9.13	4.62	8.44	10.73	7.99	*	*	-	-
	Y79AA1002416	7.52	8.19	8.76	5.47	10.72	5.8	8.2	6.05	6.59				
35	Y79AA1002429	17.73	18.61	8.81	5.82	10.24	4.73	3.65	6.89	5.66	*		-	-
	Y79AA1002431	3.38	3.05	6.2	3.01	5.89	1.6	2.81	2.79	1.69				
	Y79AA1002433	9.94	11.67	9.29	5.11	5.57	3.18	3.49	4.6	3.87	**	**	-	-
	Y79AA1002445	33.47	25.62	23.49	15.99	10.67	7.02	18.92	25.26	13.87	*		-	-
	Y79AA1002461	7.94	6.22	7.84	3.36	7.35	4.7	3.49	2.25	3.85		**	-	-
40	Y79AA1002466	778.44	339.4	681.02	542.56	499.15	369	592.67	971	768.71				
	Y79AA1002471	11.38	8.13	15.35	12.81	13.4	11.43	4.94	6.06	4.47	*	*	-	-
	Y79AA1002472	31.22	33.06	31.17	18.15	21.85	9.34	16.29	20.14	20.03	*	**	-	-
	Y79AA1002474	10.68	12.29	10.71	6.77	7.3	7.75	3.17	7.37	4.86	**	*	-	-
	Y79AA1002482	30.09	33.68	36.63	19.02	23.45	17.38	21.9	25.81	23.08	**	*	-	-
	Y79AA1002487	8.33	8.29	7.43	7.28	8.45	6.44	5.34	3.78	3.86		**	-	-
45	Y79AA1002490	143.18	106.89	117.63	56.22	71.49	57.31	59.76	51.39	52.37	**	**	-	-
	Y79AA1002493	44.75	41.56	40.36	20.64	28.52	19.33	38.02	46.19	46.7	**	*	-	-
	ZRV6C1006278	5.26	7	5.52	3.16	2.97	2.19	2.99	2.6	2.72	**	**	-	-

EXAMPLE 16

Selection of novel cDNA clones from cDNA libraries prepared by oligo-capping method

[0246] The following 54 clones were newly selected from cDNA libraries prepared by oligo-capping method, based on the criterion that the 5'-end sequence of a cDNA clone contained a coding region which was initiated with ATG codon and which encoded 50 amino acids or more:

HEMBA1000497, HEMBA1001750, HEMBA1003854, HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406, HEMBA1006650, HEMBA1006812, HEMBB1000672, HEMBB1001197, HEMBB1001871, MAMMA1001252, MAMMA1002094, NT2RM4000634, NT2RM4000657,

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NT2RM4000783, NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551, NT2RP2000660, NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095, NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776, NT2RP2005806, NT2RP2005882, NT2RP3001282, NT2RP3001723, NT2RP3002099, NT2RP3003155, NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218.

Among them, the following 23 clones was predicted to contain a coding region encoding 100 amino acids or more: HEMBA1000497, HEMBA1003854, HEMBA1004193, HEMBA1006812, HEMBB1001871, NT2RM4000657, NT2RM4001178, NT2RP2001756, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2004095, NT2RP2004920, NT2RP2005806, NT2RP3001282, NT2RP3002099, NT2RP3003155, OVARC1000724, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218. This indicates that the clones encode proteins.

[0247] Table 510 shows maximal ATGprl value determined for each clone. Since the respective maximal ATGprl values for HEMBA1006812, HEMBB1001871 and NT2RRP3001282 are higher than 0.3, the clones would be full-length. Other clones indicated below have maximal ATGprl values of 0.3 or less, and this means that the fullness ratios of the clones are low.

However, the sequences can still be full-length: HEMBA1000497, HEMBA1001750, HEMBA1003854, HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406, HEMBA1006650, HEMBB1000672, HEMBB1001197, MAMMA1001252, MAMMA1002094, NT2RM4000634, NT2RM4000657, NT2RM4000783, NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551, NT2RP2000660, NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095, NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776, NT2RP2005806, NT2RP2005882, NT2RP3001723, NT2RP3002099, NT2RP3003155, NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218

[0248] Table 511 (same as Table 2) shows SEQ ID NOs of the nucleotide sequences located at the 5'-end and 3'-end of each of the 54 clones and the corresponding plasmid clone, which was obtained herein, containing a polynucleotide as an insert. SEQ ID NO for a 5'-end sequence is indicated on the right side of the corresponding Sequence name of 5'-end sequence, and SEQ ID NO for a 3'-end sequence is indicated on the right side of the corresponding Sequence name of 3'-end sequence.

[0249] Swiss-Prot was searched for data homologous to the 5' -end sequences of the selected 54 clones, and GenBank and UniGene were searched for data homologous to the 5' -end and 3'-end sequences of the same clones. The search results are indicated as Homology search results 1-7 in the last part of this SPECIFICATION.

[0250] Based on the matching data obtained by the search, 7 clones presumably encode proteins belonging to any of the categories of secretory or membrane proteins, glycoproteins, signal transduction-associated proteins, transcription-associated proteins, disease-associated proteins, and protein synthesis- and/or protein transport-associated proteins. These were clones exhibiting relatively low homology to any of known proteins belonging to said categories. Here, the term "relatively low homology" means that a nucleotide sequence does not satisfy the conditions under which the nucleotide sequence exhibits "relatively high homology" (which means that, when the nucleotide sequence is compared with the known sequences in Swiss-Prot database, the sequence identity is 60% or higher and the P value is 10^{-10} or less) and that, when the nucleotide sequence is compared with the known sequences in Swiss-Prot database, the sequence to be compared contains 55 nucleotides or more, the sequence identity is 25% or higher, and the P value is 10^{-6} or less.

[0251] Among the 7 clones, clones presumably encoding proteins belonging to the category of secretory or membrane proteins are the two clones, HEMBB1001871 and NT2RM4000857 (which also belong to other categories); clones presumably encoding proteins belonging to the category of glycoproteins are the two clones, HEMBB1001871 and NT2RM4000857 (which also belong to other categories); a clone presumably encoding a protein belonging to the category of signal transduction-associated proteins is PLACE1005549; clones presumably encoding proteins belonging to the category of transcription-associated proteins are the three clones, HEMBA1005572, NT2RP2001756, and NT2RP2005776; a clone presumably encoding a protein belonging to the category of disease-associated proteins is NT2RM4000857 (which also belong to other categories); a clone presumably encoding a protein belonging to the category of protein synthesis- and/or protein transport-associated proteins is HEMBA1001750 (see Examples 12).

EXAMPLE 17

Search for a signal sequence, transmembrane region and functional domain in deduced amino acid sequences

5 **[0252]** The deduced amino acid sequences from the full-length nucleotide sequences were examined to predict the presence of a signal sequence in their amino-termini as well as the presence of a transmembrane region. The amino acid sequences were also searched for a protein functional domain (motif). The examinations for a signal sequence in the amino-terminus, for a transmembrane region and for a functional domain were performed by using PSORT [K. Nakai & M. Kanehisa, Genomics, 14:897-911 (1992)], SOSUI [T. Hirokawa et al., Bioinformatics, 14:378-379 (1998)]
 10 (Mitsui Knowledge Industry Co., Ltd.) and Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>), respectively. When the presence of a signal sequence or a transmembrane region in the amino-terminus was predicted in the amino acid sequence by PSORT or SOSUI, the protein was predicted to be a secretory protein or a membrane protein. When the amino acid sequence matched a functional domain in the Pfam search for a functional domain, the function of the protein is predictable based on the matching data, for example, by referring to the functional categories in PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>). The functional domain search can be performed by using PROSITE instead of Pfam.

[0253] Search results obtained by using the respective software programs are indicated below.

[0254] Clones whose deduced amino acid sequences were predicted to have signal sequences by PSORT search are as follows:

20 HEMBA1001052, HEMBA1001407, HEMBA1002486, HEMBA1002661, HEMBA1002818, HEMBA1002876,
 HEMBA1003086, HEMBA1003711, HEMBA1004752, HEMBA1005991, HEMBA1006067, HEMBA1006173,
 HEMBA1006198, HEMBA1006789, HEMBA1006921, HEMBB1000054, HEMBB1000175, HEMBB1002692,
 MAMMA1000798, MAMMA1002427, MAMMA1002881, MAMMA1003035, NT2RM1000035, NT2RM1000742,
 NT2RM1000811, NT2RM1000905, NT2RM1001008, NT2RM2000287, NT2RM2000609, NT2RM2001613,
 25 NT2RM4000634, NT2RM4000778, NT2RM4002339, NT2RM4002460, NT2RP1000782, NT2RP1000856,
 NT2RP1001247, NT2RP1001546, NT2RP1001569, NT2RP2001597, NT2RP2002537, NT2RP2004142,
 NT2RP2005752, NT2RP2005812, NT2RP3001084, NT2RP3001589, NT2RP3002163, NT2RP3002650,
 NT2RP3003145, NT2RP3003242, NT2RP3003621, NT2RP3004282, NT2RP3004503, NT2RP4000051,
 NT2RP4000151, NT2RP4000243, NT2RP4000259, NT2RP4000323, NT2RP4000417, NT2RP4001064,
 30 NT2RP4001117, NT2RP4001730, NT2RP4001739, NT2RP4002075, NT2RP5003500, OVARC1001154,
 PLACE1000611, PLACE1003030, PLACE1003044, PLACE1003369, PLACE1003596, PLACE1004258,
 PLACE1005086, PLACE1006239, PLACE1006754, PLACE1006829, PLACE1007954, PLACE1008424,
 PLACE1008533, PLACE1008693, PLACE1010622, PLACE1010942, PLACE2000176, PLACE2000341,
 PLACE2000379, PLACE2000427, PLACE2000477, PLACE4000431, PLACE4000593, THYRO1000156,
 35 THYRO1001134, THYRO1001287, Y79AA1000258, Y79AA1001874, Y79AA1002399, HEMBB1001871,
 HEMBB1001925, MAMMA1000778, MAMMA1000897, MAMMA1001080, NT2RP2004300, NT2RP3002985,
 NT2RP3003059, OVARC1000689, OVARC1000890, PLACE1005162, PLACE3000399, PLACE3000455,
 PLACE4000247, PLACE4000259, PLACE4000494

[0255] Clones whose deduced amino acid sequences were predicted to have transmembrane regions by SOSUI search are as follows:

40 HEMBA1000005, HEMBA1000356, HEMBA1000518, HEMBA1000531, HEMBA1000637, HEMBA1000719,
 HEMBA1000817, HEMBA1000822, HEMBA1000870, HEMBA1000991, HEMBA1001052, HEMBA1001085,
 HEMBA1001286, HEMBA1001351, HEMBA1001407, HEMBA1001446, HEMBA1001510, HEMBA1001515,
 HEMBA1001557, HEMBA1001746, HEMBA1002092, HEMBA1002125, HEMBA1002150, HEMBA1002166,
 45 HEMBA1002462, HEMBA1002477, HEMBA1002486, HEMBA1002609, HEMBA1002659, HEMBA1002661,
 HEMBA1002780, HEMBA1002818, HEMBA1002876, HEMBA1002921, HEMBA1003077, HEMBA1003079,
 HEMBA1003086, HEMBA1003096, HEMBA1003281, HEMBA1003286, HEMBA1003711, HEMBA1003742,
 HEMBA1003803, HEMBA1004143, HEMBA1004146, HEMBA1004341, HEMBA1004461, HEMBA1004577,
 HEMBA1004637, HEMBA1004752, HEMBA1004756, HEMBA1004850, HEMBA1004889, HEMBA1004923,
 50 HEMBA1004930, HEMBA1005029, HEMBA1005035, HEMBA1005050, HEMBA1005552, HEMBA1005588,
 HEMBA1005616, HEMBA1005991, HEMBA1006036, HEMBA1006067, HEMBA1006293, HEMBA1006492,
 HEMBA1006502, HEMBA1006659, HEMBA1006758, HEMBA1006789, HEMBA1006921, HEMBA1006926,
 HEMBA1007203, HEMBB1000050, HEMBB1000054, HEMBB1000556, HEMBB1000593, HEMBB1000631,
 HEMBB1000763, HEMBB1000827, HEMBB1000915, HEMBB1000975, HEMBB1001112, HEMBB1001177,
 55 HEMBB1001302, HEMBB1001348, HEMBB1001962, HEMBB1002142, HEMBB1002190, HEMBB1002247,
 HEMBB1002387, HEMBB1002550, HEMBB1002600, HEMBB1002692, MAMMA1000129, MAMMA1000133,
 MAMMA1000277, MAMMA1000278, MAMMA1000410, MAMMA1000416, MAMMA1000472, MAMMA1000714,
 MAMMA1000731, MAMMA1000734, MAMMA1000798, MAMMA1000842, MAMMA1000956, MAMMA1001008,

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	MAMMA1001030,	MAMMA1001139,	MAMMA1001154,	MAMMA1001388,	MAMMA1001411,	MAMMA1001487,
	MAMMA1001751,	MAMMA1001771,	MAMMA1002461,	MAMMA1002524,	MAMMA1002598,	MAMMA1002684,
	MAMMA1002769,	MAMMA1002890,	MAMMA1002938,	MAMMA1003146,	NT2RM1000035,	NT2RM1000037,
5	NT2RM1000062,	NT2RM1000131,	NT2RM1000257,	NT2RM1000260,	NT2RM1000355,	NT2RM1000648,
	NT2RM1000742,	NT2RM1000800,	NT2RM1000811,	NT2RM1000857,	NT2RM1000867,	NT2RM1000882,
	NT2RM1001008,	NT2RM1001115,	NT2RM1001139,	NT2RM2000259,	NT2RM2000395,	NT2RM2000402,
	NT2RM2000407,	NT2RM2000422,	NT2RM2000566,	NT2RM2000581,	NT2RM2000609,	NT2RM2001370,
	NT2RM2001393,	NT2RM2001499,	NT2RM2001613,	NT2RM2001648,	NT2RM2001659,	NT2RM2001671,
	NT2RM2001718,	NT2RM2001760,	NT2RM2001785,	NT2RM2001823,	NT2RM2001930,	NT2RM2001950,
10	NT2RM2001998,	NT2RM2002049,	NT2RM4000046,	NT2RM4000233,	NT2RM4000433,	NT2RM4000520,
	NT2RM4000634,	NT2RM4000674,	NT2RM4000700,	NT2RM4000764,	NT2RM4000795,	NT2RM4000820,
	NT2RM4000857,	NT2RM4001032,	NT2RM4001054,	NT2RM4001455,	NT2RM4001813,	NT2RM4001930,
	NT2RM4001987,	NT2RM4002054,	NT2RM4002073,	NT2RM4002145,	NT2RM4002146,	NT2RM4002194,
	NT2RM4002339,	NT2RM4002438,	NT2RM4002446,	NT2RM4002452,	NT2RM4002460,	NT2RM4002493,
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Y79AA1000342//Zinc finger, C2H2 type
 Y79AA1000349//Double-stranded RNA binding motif
 Y79AA1000627//Zinc finger, C2H2 type
 Y79AA1000705//Helicases conserved C-terminal domain
 5 Y79AA1000752//KH domain family of RNA binding proteins
 Y79AA1000833//Tubulin
 Y79AA1001048//Acyl-CoA dehydrogenases
 Y79AA1001391//Homeobox domain
 Y79AA1001394//ATPases associated with various cellular activities (AAA)
 10 Y79AA1001493//Ubiquitin-conjugating enzymes
 Y79AA1001613//Zinc finger, C2H2 type
 Y79AA1001874//TNFR/NGFR cysteine-rich region
 Y79AA1002027//Ubiquitin-conjugating enzymes
 Y79AA1002139//DnaJ, prokaryotic heat shock protein
 15 Y79AA1002208//Ank repeat
 Y79AA1002246//C2 domain
 Y79AA1002307//Fibronectin type III domain
 Y79AA1002472//Zinc finger, C2H2 type
 20 HEMBA1003538//CUB domain HEMBA1003645//WD domain, G-beta repeats //Src homology domain 3
 HEMBA1005206//Glutathione S-transferases.
 HEMBA1006521//Alcohol/other dehydrogenases, short chain type
 HEMBB1001482//Zinc finger, C2H2 type HEMBB1001915//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2 HEMBB1002044//Cadherin MAMMA1000183//Zinc finger, C2H2 type
 MAMMA1000897//von Willebrand factor type A domain MAMMA1001080//IG superfamily MAMMA1002498//IG
 25 superfamily MAMMA1002573//KH domain family of RNA binding proteins MAMMA1002617//Zinc finger, C2H2 type
 NT2RM1000833//eubacterial secY protein NT2RM2001797//Zinc finger, C2H2 type
 NT2RP1001013//Zinc finger, C2H2 type NT2RP2001233//Zinc finger, C2H2 type
 NT2RP2001440//14-3-3 proteins NT2RP2002105//7 transmembrane receptor (rhodopsin family)
 NT2RP3001723//Laminin G domain NT2RP3001938//Eukaryotic protein kinase domain NT2RP3002330//Elongation factor Tu family (contains ATP/GTP binding P-loop) NT2RP3003133//Zinc finger, C2H2 type
 30 NT2RP3003500//Eukaryotic protein kinase domain NT2RP3003799//C2 domain
 NT2RP3003800//Eukaryotic protein kinase domain NT2RP3004013//Double-stranded RNA binding motif
 NT2RP3004125//Zinc finger, C2H2 type
 OVARC1001244//Bromodomain OVARC1001496//D-isomer specific 2-hydroxyacid dehydrogenases
 35 PLACE1000007//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2
 PLACE1001118//Zinc finger, C2H2 type PLACE1010310//Zinc finger, C2H2 type PLACE1011896//wnt family of developmental signaling proteins PLACE3000124//Src homology domain 2
 PLACE4000100//D-isomer specific 2-hydroxyacid dehydrogenases
 PLACE4000259//Helicases conserved C-terminal domain PLACE4000261//Bromodomain SKNMC1000013//ABC
 40 transporters SKNMC1000091//Basic region plus leucine zipper transcription factors THYRO1000343//Src homology domain 3 THYRO1000569//Zinc finger, C2H2 type THYRO1001189//Zinc finger, C2H2 type Y79AA1002103//Zinc finger, C2H2 type PLACE3000350//Eukaryotic protein kinase domain
 PLACE4000156//Zinc finger, C2H2 type

45 EXAMPLE 18

Classification of cDNA clones into functional categories based on the full-length nucleotide sequences

50 **[0257]** Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based on the results of homology search (see Homology search results 6, 12, 13 and 14) of the databases, GenBank, Swiss-Prot and UniGene, for the full-length nucleotide sequences of 4997 clones and based on the results of domain search (see Example 17) of the deduced amino acid sequences encoded by the full-length nucleotide sequences. The target 4997 clones are listed below:

55 HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000030, HEMBA1000042, HEMBA1000046,
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 HEMBA1000158, HEMBA1000168, HEMBA1000185, HEMBA1000193, HEMBA1000201, HEMBA1000213,
 HEMBA1000216, HEMBA1000227, HEMBA1000231, HEMBA1000243, HEMBA1000244, HEMBA1000251,
 HEMBA1000264, HEMBA1000280, HEMBA1000282, HEMBA1000288, HEMBA1000290, HEMBA1000302,

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	HEMBA1000303,	HEMBA1000304,	HEMBA1000307,	HEMBA1000327,	HEMBA1000333,	HEMBA1000338,
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	HEMBA1000392,	HEMBA1000396,	HEMBA1000411,	HEMBA1000428,	HEMBA1000442,	HEMBA1000456,
	HEMBA1000459,	HEMBA1000460,	HEMBA1000469,	HEMBA1000488,	HEMBA1000491,	HEMBA1000497,
5	HEMBA1000501,	HEMBA1000504,	HEMBA1000505,	HEMBA1000508,	HEMBA1000518,	HEMBA1000519,
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	THYRO1000558,	THYRO1000569,	THYRO1000570,	THYRO1000585,	THYRO1000596,	THYRO1000605,
	THYRO1000625,	THYRO1000637,	THYRO1000662,	THYRO1000666,	THYRO1000676,	THYRO1000684,
	THYRO1000712,	THYRO1000715,	THYRO1000734,	THYRO1000748,	THYRO1000756,	THYRO1000777,
40	THYRO1000783,	THYRO1000787,	THYRO1000793,	THYRO1000796,	THYRO1000805,	THYRO1000815,
	THYRO1000843,	THYRO1000852,	THYRO1000855,	THYRO1000865,	THYRO1000895,	THYRO1000916,
	THYRO1000926,	THYRO1000934,	THYRO1000951,	THYRO1000952,	THYRO1000983,	THYRO1000988,
	THYRO1001003,	THYRO1001031,	THYRO1001033,	THYRO1001062,	THYRO1001100,	THYRO1001120,
	THYRO1001133,	THYRO1001134,	THYRO1001142,	THYRO1001173,	THYRO1001189,	THYRO1001204,
45	THYRO1001213,	THYRO1001262,	THYRO1001271,	THYRO1001287,	THYRO1001313,	THYRO1001320,
	THYRO1001321,	THYRO1001322,	THYRO1001347,	THYRO1001363,	THYRO1001365,	THYRO1001374,
	THYRO1001401,	THYRO1001403,	THYRO1001405,	THYRO1001406,	THYRO1001411,	THYRO1001426,
	THYRO1001434,	THYRO1001458,	THYRO1001480,	THYRO1001487,	THYRO1001534,	THYRO1001537,
	THYRO1001541,	THYRO1001559,	THYRO1001570,	THYRO1001584,	THYRO1001595,	THYRO1001602,
50	THYRO1001605,	THYRO1001617,	THYRO1001637,	THYRO1001656,	THYRO1001661,	THYRO1001671,
	THYRO1001673,	THYRO1001703,	THYRO1001706,	THYRO1001721,	THYRO1001738,	THYRO1001745,
	THYRO1001746,	THYRO1001772,	THYRO1001793,	THYRO1001809,	THYRO1001828,	THYRO1001854,
	THYRO1001895,	THYRO1001907,	VESEN1000122,	Y79AA1000013,	Y79AA1000033,	Y79AA1000037,
	Y79AA1000059,	Y79AA1000065,	Y79AA1000131,	Y79AA1000181,	Y79AA1000202,	Y79AA1000214,
55	Y79AA1000230,	Y79AA1000231,	Y79AA1000258,	Y79AA1000268,	Y79AA1000313,	Y79AA1000328,
	Y79AA1000342,	Y79AA1000346,	Y79AA1000349,	Y79AA1000355,	Y79AA1000368,	Y79AA1000410,
	Y79AA1000420,	Y79AA1000469,	Y79AA1000480,	Y79AA1000539,	Y79AA1000540,	Y79AA1000560,
	Y79AA1000574,	Y79AA1000589,	Y79AA1000627,	Y79AA1000705,	Y79AA1000734,	Y79AA1000748,

	Y79AA1000752,	Y79AA1000774,	Y79AA1000782,	Y79AA1000784,	Y79AA1000794,	Y79AA1000800,
	Y79AA1000802,	Y79AA1000805,	Y79AA1000824,	Y79AA1000827,	Y79AA1000833,	Y79AA1000850,
	Y79AA1000962,	Y79AA1000966,	Y79AA1000968,	Y79AA1000969,	Y79AA1000976,	Y79AA1000985,
	Y79AA1001023,	Y79AA1001041,	Y79AA1001048,	Y79AA1001061,	Y79AA1001068,	Y79AA1001077,
5	Y79AA1001078,	Y79AA1001145,	Y79AA1001167,	Y79AA1001177,	Y79AA1001185,	Y79AA1001211,
	Y79AA1001216,	Y79AA1001228,	Y79AA1001233,	Y79AA1001236,	Y79AA1001281,	Y79AA1001299,
	Y79AA1001312,	Y79AA1001323,	Y79AA1001384,	Y79AA1001391,	Y79AA1001394,	Y79AA1001402,
	Y79AA1001493,	Y79AA1001511,	Y79AA1001533,	Y79AA1001541,	Y79AA1001548,	Y79AA1001555,
	Y79AA1001581,	Y79AA1001585,	Y79AA1001594,	Y79AA1001603,	Y79AA1001613,	Y79AA1001647,
10	Y79AA1001665,	Y79AA1001679,	Y79AA1001692,	Y79AA1001696,	Y79AA1001705,	Y79AA1001711,
	Y79AA1001781,	Y79AA1001805,	Y79AA1001827,	Y79AA1001846,	Y79AA1001866,	Y79AA1001874,
	Y79AA1001875,	Y79AA1001923,	Y79AA1001963,	Y79AA1002027,	Y79AA1002083,	Y79AA1002089,
	Y79AA1002103,	Y79AA1002115,	Y79AA1002125,	Y79AA1002139,	Y79AA1002204,	Y79AA1002208,
	Y79AA1002209,	Y79AA1002210,	Y79AA1002211,	Y79AA1002220,	Y79AA1002229,	Y79AA1002234,
15	Y79AA1002246,	Y79AA1002258,	Y79AA1002298,	Y79AA1002307,	Y79AA1002311,	Y79AA1002351,
	Y79AA1002361,	Y79AA1002399,	Y79AA1002407,	Y79AA1002416,	Y79AA1002431,	Y79AA1002433,
	Y79AA1002472,	Y79AA1002482,	Y79AA1002487,			

[0258] Among the 4997 clones, there are 2189 clones that presumably encode proteins belonging to any of the categories of secretory or membrane proteins, glycoprotein-associated proteins, signal transduction-associated proteins, transcription-associated proteins, disease-associated proteins, enzymes and/or metabolism-associated proteins, ATP- and/or GTP-binding proteins, nuclear proteins, DNA- and/or RNA-binding proteins, RNA synthesis-associated proteins, protein synthesis- and/or protein transport-associated proteins, cytoskeleton-associated proteins, cell division- and/or cell proliferation-associated proteins, embryogenesis- and/or development-associated proteins, or cellular defense-associated proteins.

[0259] The clones that presumably encode proteins belonging to the category of secretory or membrane proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "growth factor", "cytokine", "hormone", "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen", or "connective tissue"; those which matched the data, suggesting that the proteins are secretory or membrane proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description; and, further, those predicted to have an N-terminal signal sequence or a transmembrane region as a result of domain search for the amino acid sequences deduced from the full-length nucleotide sequences.

[0260] The clones that presumably encode proteins belonging to the category of glycoprotein-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "glycoprotein"; those which matched the data, suggesting that the proteins are glycoprotein; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0261] The clones that presumably encode proteins belonging to the category of signal transduction-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "serine/threonine-protein kinase", "tyrosine-protein kinase", or "SH3 domain"; those which matched the data, suggesting that the proteins are signal transduction-associated proteins (for example, "ADP-ribosylation factor"); or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0262] The clones that presumably encode proteins belonging to the category of transcription-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "transcription regulation", "zinc finger", or "homeobox"; those which matched the data, suggesting that the proteins are transcription-associated proteins; or those which matched the full-length sequences of GenBank or UniGene database with similar description.

[0263] The clones that presumably encode proteins belonging to the category of disease-associated proteins are those which matched the full-length sequences of Swiss-Prot database with the keywords "disease mutation" or "syndrome"; those which matched the data, suggesting that the proteins are disease-associated proteins; or those which matched the full-length sequences of Swiss-Prot database and GenBank or UniGene database where the matched sequences of genes or proteins which had been registered in the database of Online Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is a database of human genes and diseases.

[0264] The clones that presumably encode proteins belonging to the category of enzymes and/or metabolism-associated proteins are those which showed the terms "metabolism", "oxidoreductase", or "E.C. No. (Enzyme commission number)" in the matching data.

[0265] The clones that presumably encode proteins belonging to the category of ATP- and/or GTP-binding proteins are those which matched the data with the terms "ATP-binding" or "GTP-binding".

[0266] The clones that presumably encode proteins belonging to the category of nuclear proteins are those which matched the data with the terms "nuclear protein".

[0267] The clones that presumably encode proteins belonging to the category of DNA- and/or RNA-binding proteins are those which matched the data with the terms "DNA-binding" or "RNA-binding".

[0268] The clones that presumably encode proteins belonging to the category of RNA synthesis-associated proteins are those which matched the data with the terms "RNA splicing", "RNA processing", "RNA helicase", or "polyadenylation".

[0269] The clones that presumably encode proteins belonging to the category of protein synthesis- and/or protein transport-associated proteins are those which matched the data with the terms "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", "protein transport", or "signal recognition particle".

[0270] The clones that presumably encode proteins belonging to the category of cytoskeleton-associated proteins are those which matched the data with the terms "structural protein", "cytoskeleton", "actin-binding", or "microtubules".

[0271] The clones that presumably encode proteins belonging to the category of cell division- and/or cell proliferation-associated proteins are those which matched the data with the terms "cell division", "cell cycle", "mitosis", "chromosomal protein", "cell growth", or "apoptosis".

[0272] The clones that presumably encode proteins belonging to the category of embryogenesis- and/or development-associated proteins are those which matched the data with the terms "developmental protein".

[0273] The clones that presumably encode proteins belonging to the category of cellular defense-associated proteins are those which matched the data with the terms "heat shock", "DNA repair", or "DNA damage".

[0274] When a clone belonged to the above-mentioned multiple functional categories, the clone was classified into the multiple categories. However, the functions of the protein encoded by the clone are not limited to the functions of the categories into which the clone was classified, and therefore, additional functions can be found for the protein by further analyses.

[0275] The following 796 clones are categorized into secretory or membrane proteins.

HEMBA1000356,	HEMBA1000518,	HEMBA1000531,	HEMBA1000637,	HEMBA1000719,	HEMBA1000817,
HEMBA1000822,	HEMBA1000852,	HEMBA1000870,	HEMBA1000991,	HEMBA1001052,	HEMBA1001071,
HEMBA1001085,	HEMBA1001286,	HEMBA1001351,	HEMBA1001407,	HEMBA1001446,	HEMBA1001515,
HEMBA1001557,	HEMBA1001569,	HEMBA1001661,	HEMBA1001734,	HEMBA1001746,	HEMBA1001866,
HEMBA1002125,	HEMBA1002150,	HEMBA1002166,	HEMBA1002417,	HEMBA1002462,	HEMBA1002475,
HEMBA1002477,	HEMBA1002486,	HEMBA1002609,	HEMBA1002659,	HEMBA1002661,	HEMBA1002780,
HEMBA1002818,	HEMBA1002876,	HEMBA1002921,	HEMBA1003071,	HEMBA1003077,	HEMBA1003079,
HEMBA1003086,	HEMBA1003096,	HEMBA1003281,	HEMBA1003286,	HEMBA1003538,	HEMBA1003711,
HEMBA1003742,	HEMBA1003803,	HEMBA1004055,	HEMBA1004143,	HEMBA1004146,	HEMBA1004207,
HEMBA1004341,	HEMBA1004461,	HEMBA1004577,	HEMBA1004637,	HEMBA1004752,	HEMBA1004756,
HEMBA1004850,	HEMBA1004889,	HEMBA1004923,	HEMBA1004930,	HEMBA1005029,	HEMBA1005035,
HEMBA1005050,	HEMBA1005552,	HEMBA1005576,	HEMBA1005581,	HEMBA1005588,	HEMBA1005616,
HEMBA1005699,	HEMBA1005991,	HEMBA1006036,	HEMBA1006038,	HEMBA1006067,	HEMBA1006173,
HEMBA1006198,	HEMBA1006293,	HEMBA1006310,	HEMBA1006492,	HEMBA1006502,	HEMBA1006583,
HEMBA1006659,	HEMBA1006758,	HEMBA1006789,	HEMBA1006921,	HEMBA1006926,	HEMBA1006976,
HEMBA1007203,	HEMBA1007301,	HEMBA1000037,	HEMBA1000050,	HEMBA1000054,	HEMBA1000175,
HEMBA1000317,	HEMBA1000556,	HEMBA1000593,	HEMBA1000631,	HEMBA1000763,	HEMBA1000827,
HEMBA1000915,	HEMBA1000975,	HEMBA1001112,	HEMBA1001151,	HEMBA1001177,	HEMBA1001302,
HEMBA1001348,	HEMBA1001564,	HEMBA1001630,	HEMBA1001871,	HEMBA1001872,	HEMBA1001925,
HEMBA1001962,	HEMBA1002042,	HEMBA1002044,	HEMBA1002142,	HEMBA1002190,	HEMBA1002193,
HEMBA1002247,	HEMBA1002383,	HEMBA1002387,	HEMBA1002550,	HEMBA1002600,	HEMBA1002692,
MAMMA1000045,	MAMMA1000129,	MAMMA1000133,	MAMMA1000277,	MAMMA1000278,	MAMMA1000410,
MAMMA1000416,	MAMMA1000472,	MAMMA1000672,	MAMMA1000684,	MAMMA1000714,	MAMMA1000734,
MAMMA1000778,	MAMMA1000798,	MAMMA1000842,	MAMMA1000859,	MAMMA1000897,	MAMMA1000956,
MAMMA1001008,	MAMMA1001030,	MAMMA1001041,	MAMMA1001073,	MAMMA1001080,	MAMMA1001139,
MAMMA1001154,	MAMMA1001322,	MAMMA1001388,	MAMMA1001411,	MAMMA1001487,	MAMMA1001751,
MAMMA1001754,	MAMMA1001771,	MAMMA1002009,	MAMMA1002427,	MAMMA1002428,	MAMMA1002461,
MAMMA1002524,	MAMMA1002573,	MAMMA1002598,	MAMMA1002655,	MAMMA1002684,	MAMMA1002769,
MAMMA1002844,	MAMMA1002881,	MAMMA1002890,	MAMMA1002938,	MAMMA1002947,	MAMMA1003035,
MAMMA1003089,	MAMMA1003146,	MAMMA1003150,	NT2RM1000035,	NT2RM1000037,	NT2RM1000062,
NT2RM1000080,	NT2RM1000092,	NT2RM1000131,	NT2RM1000199,	NT2RM1000257,	NT2RM1000260,
NT2RM1000355,	NT2RM1000430,	NT2RM1000563,	NT2RM1000648,	NT2RM1000742,	NT2RM1000770,
NT2RM1000800,	NT2RM1000811,	NT2RM1000833,	NT2RM1000857,	NT2RM1000867,	NT2RM1000882,
NT2RM1000905,	NT2RM1001008,				
NT2RM1001115,	NT2RM1001139,	NT2RM2000259,	NT2RM2000260,	NT2RM2000287,	NT2RM2000395,
NT2RM2000402,	NT2RM2000407,	NT2RM2000422,	NT2RM2000490,	NT2RM2000522,	NT2RM2000566,

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	NT2RM2000581,	NT2RM2000609,	NT2RM2000821,	NT2RM2001370,	NT2RM2001393,	NT2RM2001499,
	NT2RM2001547,	NT2RM2001613,	NT2RM2001648,	NT2RM2001659,	NT2RM2001671,	NT2RM2001688,
	NT2RM2001698,	NT2RM2001718,	NT2RM2001753,	NT2RM2001760,	NT2RM2001785,	NT2RM2001930,
	NT2RM2001950,	NT2RM2001997,	NT2RM2001998,	NT2RM2002049,	NT2RM2002145,	NT2RM4000233,
5	NT2RM4000433,	NT2RM4000457,	NT2RM4000486,	NT2RM4000496,	NT2RM4000520,	NT2RM4000634,
	NT2RM4000674,	NT2RM4000700,	NT2RM4000764,	NT2RM4000778,	NT2RM4000795,	NT2RM4000820,
	NT2RM4000857,	NT2RM4001032,	NT2RM4001054,	NT2RM4001116,	NT2RM4001455,	NT2RM4001666,
	NT2RM4001810,	NT2RM4001813,	NT2RM4001930,	NT2RM4001987,	NT2RM4002054,	NT2RM4002073,
	NT2RM4002145,	NT2RM4002146,	NT2RM4002189,	NT2RM4002194,	NT2RM4002251,	NT2RM4002339,
10	NT2RM4002438,	NT2RM4002446,	NT2RM4002452,	NT2RM4002460,	NT2RM4002493,	NT2RM4002558,
	NT2RM4002565,	NT2RM4002571,	NT2RM4002594,	NT2RP1000130,	NT2RP1000191,	NT2RP1000326,
	NT2RP1000358,	NT2RP1000413,	NT2RP1000418,	NT2RP1000547,	NT2RP1000609,	NT2RP1000677,
	NT2RP1000767,	NT2RP1000782,	NT2RP1000856,	NT2RP1001113,	NT2RP1001247,	NT2RP1001286,
	NT2RP1001310,	NT2RP1001311,	NT2RP1001313,	NT2RP1001385,	NT2RP1001449,	NT2RP1001546,
15	NT2RP1001569,	NT2RP2000032,	NT2RP2000040,	NT2RP2000056,	NT2RP2000070,	NT2RP2000091,
	NT2RP2000114,	NT2RP2000120,	NT2RP2000173,	NT2RP2000175,	NT2RP2000195,	NT2RP2000257,
	NT2RP2000270,	NT2RP2000283,	NT2RP2000288,	NT2RP2000289,	NT2RP2000459,	NT2RP2000516,
	NT2RP2000660,	NT2RP2000842,	NT2RP2000892,	NT2RP2001081,	NT2RP2001268,	NT2RP2001295,
	NT2RP2001366,	NT2RP2001378,	NT2RP2001576,	NT2RP2001581,	NT2RP2001597,	NT2RP2001613,
20	NT2RP2001947,	NT2RP2001991,	NT2RP2002025,	NT2RP2002066,	NT2RP2002078,	NT2RP2002105,
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	NT2RP2003446,	NT2RP2003466,	NT2RP2003506,	NT2RP2003513,	NT2RP2003629,	NT2RP2003668,
	NT2RP2003760,	NT2RP2003777,	NT2RP2003781,	NT2RP2004041,	NT2RP2004142,	NT2RP2004194,
25	NT2RP2004270,	NT2RP2004300,	NT2RP2004392,	NT2RP2004655,	NT2RP2004681,	NT2RP2004775,
	NT2RP2004799,	NT2RP2004936,	NT2RP2004959,	NT2RP2005012,	NT2RP2005159,	NT2RP2005227,
	NT2RP2005270,	NT2RP2005344,	NT2RP2005465,	NT2RP2005509,	NT2RP2005752,	NT2RP2005781,
	NT2RP2005784,	NT2RP2005812,	NT2RP2006069,	NT2RP2006100,	NT2RP2006141,	NT2RP2006184,
	NT2RP2006261,	NT2RP2006565,	NT2RP2006571,	NT2RP2006573,	NT2RP3000092,	NT2RP3000109,
30	NT2RP3000134,	NT2RP3000207,	NT2RP3000333,	NT2RP3000341,	NT2RP3000393,	NT2RP3000439,
	NT2RP3000441,	NT2RP3000531,	NT2RP3000685,	NT2RP3000825,	NT2RP3000826,	NT2RP3000852,
	NT2RP3000919,	NT2RP3001084,	NT2RP3001096,	NT2RP3001126,	NT2RP3001140,	NT2RP3001176,
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	NT2RP3002007,	NT2RP3002014,	NT2RP3002054,	NT2RP3002108,	NT2RP3002163,	NT2RP3002351,
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40	NT2RP3003242,	NT2RP3003302,	NT2RP3003353,	NT2RP3003409,	NT2RP3003576,	NT2RP3003621,
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45	NT2RP4000417,	NT2RP4000500,	NT2RP4000524,	NT2RP4000556,	NT2RP4000560,	NT2RP4000588,
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50	NT2RP4001379,	NT2RP4001498,	NT2RP4001547,	NT2RP4001571,	NT2RP4001574,	NT2RP4001644,
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	NT2RP4001823,	NT2RP4001950,	NT2RP4001975,	NT2RP4002052,	NT2RP4002075,	NT2RP5003500,
	NT2RP5003506,	NT2RP5003522,	NT2RP5003534,	OVARC1000060,	OVARC1000335,	OVARC1000682,
	OVARC1000689,	OVARC1000700,	OVARC1000722,	OVARC1000751,	OVARC1000850,	OVARC1000890,
55	OVARC1000924,	OVARC1000936,	OVARC1000959,	OVARC1000984,	OVARC1000999,	OVARC1001034,
	OVARC1001055,	OVARC1001117,	OVARC1001129,	OVARC1001154,	OVARC1001329,	OVARC1001381,
	OVARC1001391,	OVARC1001453,	OVARC1001476,	OVARC1001506,	OVARC1001610,	OVARC1001702,
	OVARC1001703,	OVARC1001713,	OVARC1001745,	OVARC1001767,	OVARC1002127,	OVARC1002138,

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	OVARC1002158,	OVARC1002165,	PLACE1000014,	PLACE1000213,	PLACE1000401,	PLACE1000562,
	PLACE1000611,	PLACE1000656,	PLACE1000712,	PLACE1 000793,	PLACE1000909,	PLACE1000948,
	PLACE1000977,	PLACE1001241,	PLACE1001257,	PLACE1001377,	PLACE1001517,	PLACE1001610,
5	PLACE1001761,	PLACE1001771,	PLACE1001817,	PLACE1001983,	PLACE1002046,	PLACE1002140,
	PLACE1002213,	PLACE1002395,	PLACE1002437,	PLACE1002500,	PLACE1002583,	PLACE1002714,
	PLACE1002722,	PLACE1002782,	PLACE1002794,	PLACE1002851,	PLACE1002908,	PLACE1003030,
	PLACE1003044,	PLACE1003045,	PLACE1003238,	PLACE1003296,	PLACE1003369,	PLACE1003420,
	PLACE1003493,	PLACE1003537,	PLACE1003553,	PLACE1003596,	PLACE1003760,	PLACE1003768,
10	PLACE1003771,	PLACE1003903,	PLACE1004149,	PLACE1004197,	PLACE1004203,	PLACE1004258,
	PLACE1004270,	PLACE1004277,	PLACE1004289,	PLACE1004473,	PLACE1004629,	PLACE1004646,
	PLACE1004743,	PLACE1004751,	PLACE1004793,	PLACE1004840,	PLACE1004969,	PLACE1005086,
	PLACE1005162,	PLACE1005206,	PLACE1005313,	PLACE1005467,	PLACE1005530,	PLACE1005595,
	PLACE1005611,	PLACE1005623,	PLACE1005763,	PLACE1005884,	PLACE1005890,	PLACE1005898,
15	PLACE1005934,	PLACE1005953,	PLACE1006157,	PLACE1006225,	PLACE1006239,	PLACE1006288,
	PLACE1006492,	PLACE1006534,	PLACE1006678,	PLACE1006754,	PLACE1006901,	PLACE1006935,
	PLACE1006956,	PLACE1007111,	PLACE1007243,	PLACE1007274,	PLACE1007282,	PLACE1007317,
	PLACE1007375,	PLACE1007386,	PLACE1007409,	PLACE1007416,	PLACE1007484,	PLACE1007583,
	PLACE1007632,	PLACE1007645,	PLACE1007649,	PLACE1007852,	PLACE1007877,	PLACE1007954,
20	PLACE1008273,	PLACE1008309,	PLACE1008331,	PLACE1008402,	PLACE1008424,	PLACE1008429,
	PLACE1008531,	PLACE1008532,	PLACE1008533,	PLACE1008568,	PLACE1008643,	PLACE1008693,
	PLACE1008715,	PLACE1009045,	PLACE1009094,	PLACE1009298,	PLACE1009319,	PLACE1009338,
	PLACE1009368,	PLACE1009493,	PLACE1009639,	PLACE1009659,	PLACE1009708,	PLACE1009731,
	PLACE1009845,	PLACE1009861,	PLACE1009935,	PLACE1009992,	PLACE1010089,	PLACE1010231,
25	PLACE1010321,	PLACE1010362,	PLACE1010599,	PLACE1010622,	PLACE1010662,	PLACE1010811,
	PLACE1010917,	PLACE1010942,	PLACE1010954,	PLACE1011090,	PLACE1011214,	PLACE1011221,
	PLACE1011371,	PLACE1011399,	PLACE1011492,	PLACE1011646,	PLACE1011749,	PLACE1011896,
	PLACE2000034,	PLACE2000062,	PLACE2000111,	PLACE2000132,	PLACE2000176,	PLACE2000187,
	PLACE2000216,	PLACE2000335,	PLACE2000341,	PLACE2000373,	PLACE2000379,	PLACE2000398,
30	PLACE2000399,	PLACE2000425,	PLACE2000438,	PLACE2000458,	PLACE2000477,	PLACE3000020,
	PLACE3000218,	PLACE3000226,	PLACE3000242,	PLACE3000244,	PLACE3000339,	PLACE3000373,
	PLACE3000399,	PLACE3000406,	PLACE3000413,	PLACE3000455,	PLACE4000052,	PLACE4000063,
	PLACE4000129,	PLACE4000247,	PLACE4000250,	PLACE4000259,	PLACE4000300,	PLACE4000387,
	PLACE4000431,	PLACE4000487,	PLACE4000494,	PLACE4000522,	PLACE4000548,	PLACE4000581,
35	PLACE4000593,	PLACE4000650,	THYRO1000156,	THYRO1000327,	THYRO1000394,	THYRO1000395,
	THYRO1000570,	THYRO1000748,	THYRO1000756,	THYRO1000783,	THYRO1001134,	THYRO1001271,
	THYRO1001287,	THYRO1001320,	THYRO1001401,	THYRO1001534,	THYRO1001537,	THYRO1001541,
	THYRO1001828,	Y79AA1000258,	Y79AA1000420,	Y79AA1000469,	Y79AA1000734,	Y79AA1000800,
	Y79AA1000976,	Y79AA1001023,	Y79AA1001177,	Y79AA1001384,	Y79AA1001394,	Y79AA1001603,
	Y79AA1001647,	Y79AA1001846,	Y79AA1001874,	Y79AA1002139,	Y79AA1002246,	Y79AA1002351,
40	Y79AA1002399,	Y79AA1002416,				

[0276] The following 141 clones are categorized into glycoproteins-associated proteins.

	HEMBA1000156,	HEMBA1000518,	HEMBA1000852,	HEMBA1001071,	HEMBA1001286,	HEMBA1001661,
	HEMBA1001734,	HEMBA1001866,	HEMBA1003071,	HEMBA1003077,	HEMBA1003281,	HEMBA1003538,
	HEMBA1003679,	HEMBA1003866,	HEMBA1005576,	HEMBA1005581,	HEMBA1005699,	HEMBA1006038,
45	HEMBA1006976,	HEMBA1007301,	HEMBA1000317,	HEMBA1000915,	HEMBA1001871,	HEMBA1001872,
	HEMBA1002193,	MAMMA1000672,	MAMMA1000897,	MAMMA1001030,	MAMMA1001388,	MAMMA1002329,
	MAMMA1002428,	MAMMA1002573,	MAMMA1003150,	NT2RM1000648,	NT2RM1001115,	NT2RM2000260,
	NT2RM2000407,	NT2RM2000422,	NT2RM2000490,	NT2RM2001499,	NT2RM2001659,	NT2RM2001930,
	NT2RM4000820,	NT2RM4000857,	NT2RM4001810,	NT2RM4001813,	NT2RM4001987,	NT2RM4002145,
50	NT2RM4002189,	NT2RM4002251,	NT2RM4002460,	NT2RM4002558,	NT2RP1000677,	NT2RP1000782,
	NT2RP1000856,	NT2RP1001546,	NT2RP2000056,	NT2RP2000070,	NT2RP2001295,	NT2RP2001378,
	NT2RP2001597,	NT2RP2001991,	NT2RP2002025,	NT2RP2002078,	NT2RP2002385,	NT2RP2004587,
	NT2RP2004732,	NT2RP2005531,	NT2RP3000207,	NT2RP3000531,	NT2RP3000825,	NT2RP3001140,
	NT2RP3002810,	NT2RP3003672,	NT2RP3003701,	NT2RP3003716,	NT2RP3003914,	NT2RP3004148,
55	NT2RP4000212,	NT2RP4000417,	NT2RP4000724,	NT2RP4000817,	NT2RP4000925,	NT2RP4001150,
	NT2RP4001372,	NT2RP4001730,	NT2RP4001822,	NT2RP4001823,	NT2RP5003522,	OVARC1000091,
	OVARC1000288,	OVARC1000682,	OVARC1001055,	OVARC1001506,	OVARC1001713,	OVARC1002127,
	PLACE1000213,	PLACE1000401,	PLACE1002437,	PLACE1002583,		

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	PLACE1002722,	PLACE1003045,	PLACE1003238,	PLACE1003258,	PLACE1003493,	PLACE1004197,
	PLACE1004793,	PLACE1005953,	PLACE1005955,	PLACE1006157,	PLACE1006239,	PLACE1006368,
	PLACE1006534,	PLACE1006754,	PLACE1006956,	PLACE1007416,	PLACE1007632,	PLACE1007649,
	PLACE1008643,	PLACE1009094,	PLACE1009992,	PLACE1010231,	PLACE1010662,	PLACE1011371,
5	PLACE2000034,	PLACE2000373,	PLACE2000398,	PLACE2000399,	PLACE2000438,	PLACE2000458,
	PLACE3000339,	PLACE4000063,	PLACE4000230,	PLACE4000522,	PLACE4000548,	PLACE4000581,
	THYRO1000327, THYRO1000756, THYRO1001287, Y79AA1001603, Y79AA1001874					
	[0277] The following 129 clones are categorized into signal transduction-associated proteins.					
	HEMBA1000303,	HEMBA1000369,	HEMBA1000608,	HEMBA1000657,	HEMBA1000919,	HEMBA1001019,
10	HEMBA1001174,	HEMBA1001822,	HEMBA1001921,	HEMBA1002139,	HEMBA1002212,	HEMBA1002341,
	HEMBA1002417,	HEMBA1002768,	HEMBA1003250,	HEMBA1003291,	HEMBA1003645,	HEMBA1004286,
	HEMBA1005737,	HEMBA1006130,	HEMBA1006708,	HEMBB1000083,	HEMBB1000266,	HEMBB1000632,
	HEMBB1000781,	HEMBB1000831,	HEMBB1002193,	MAMMA1000173,	MAMMA1001038,	MAMMA1001198,
	MAMMA1002842,	MAMMA1003057,	NT2RM1000702,	NT2RM1000772,	NT2RM1001072,	NT2RM2000030,
15	NT2RM2000469,	NT2RM2000612,	NT2RM2001221,	NT2RM2001345,	NT2RM2002128,	NT2RM4000229,
	NT2RM4000354,	NT2RM4000611,	NT2RM4000798,	NT2RM4001411,	NT2RM4001412,	NT2RM4001629,
	NT2RM4001758,	NT2RM4002013,	NT2RM4002527,	NT2RP1000018,	NT2RP1000701,	NT2RP1001294,
	NT2RP1001302,	NT2RP2000668,	NT2RP2001440,	NT2RP2001560,	NT2RP2002058,	NT2RP2002193,
	NT2RP2002408,	NT2RP2002710,	NT2RP2002929,	NT2RP2003164,	NT2RP2003912,	NT2RP2004232,
20	NT2RP2004768,	NT2RP2006071,	NT2RP2006534,	NT2RP3000759,	NT2RP3000845,	NT2RP3001646,
	NT2RP3001857,	NT2RP3001938,	NT2RP3002004,	NT2RP3002785,	NT2RP3002909,	NT2RP3002988,
	NT2RP3003800,	NT2RP3004189,	NT2RP3004544,	NT2RP4000147,	NT2RP4000839,	NT2RP4001122,
	NT2RP4001148,	NT2RP4001336,	NT2RP4001375,	NT2RP4001644,	NT2RP4001725,	NT2RP4001849,
	NT2RP4001896,	NT2RP4001927,	NT2RP4002408,	NT2RP5003477,	OVARC1000013,	OVARC1000437,
25	OVARC1000556,	OVARC1000649,	OVARC 1000945,	OVARC1001200,	OVARC1002182,	PLACE1000977,
	PLACE1001387,	PLACE1002493,	PLACE1002591,	PLACE1003190,	PLACE1003353,	PLACE1004128,
	PLACE1004302,	PLACE1004937,	PLACE1005243,	PLACE1008000,	PLACE1008244,	PLACE1008650,
	PLACE1009468,	PLACE1009596,	PLACE1009708,	PLACE1009845,	PLACE1010926,	PLACE1011041,
	PLACE2000164,	PLACE2000371,	PLACE3000145,	PLACE3000350,	THYRO1000072,	THYRO1000748,
30	THYRO1001120, Y79AA1000328, Y79AA1002431					
	[0278] The following 309 clones are categorized into transcription -associated proteins.					
	HEMBA1000158,	HEMBA1000201,	HEMBA1000216,	HEMBA1000555,	HEMBA1000561,	HEMBA1000851,
	HEMBA1001077,	HEMBA1001137,	HEMBA1001405,	HEMBA1001510,	HEMBA1001635,	HEMBA1001804,
	HEMBA1001809,	HEMBA1001819,	HEMBA1001847,	HEMBA1001869,	HEMBA1002035,	HEMBA1002092,
35	HEMBA1002177,	HEMBA1002770,	HEMBA1002935,	HEMBA1003408,	HEMBA1003545,	HEMBA1003568,
	HEMBA1003662,	HEMBA1003684,	HEMBA1003760,	HEMBA1003953,	HEMBA1004097,	HEMBA1004321,
	HEMBA1004353,	HEMBA1004389,	HEMBA1004479,	HEMBA1004758,	HEMBA1004973,	HEMBA1005219,
	HEMBA1005359,	HEMBA1005513,	HEMBA1005528,	HEMBA1005548,	HEMBA1005558,	HEMBA1005931,
	HEMBA1006158,	HEMBA1006248,	HEMBA1006278,	HEMBA1006283,	HEMBA1006347,	HEMBA1006359,
40	HEMBA1006559,	HEMBA1006941,	HEMBB1000789,	HEMBB1001011,	HEMBB1001314,	HEMBB1001482,
	HEMBB1001673,	HEMBB1001749,	HEMBB1001839,	HEMBB1001908,	HEMBB1002134,	HEMBB1002217,
	HEMBB1002342,	HEMBB1002607,	MAMMA1000183,	MAMMA1000388,	MAMMA1001105,	MAMMA1001222,
	MAMMA1001260,	MAMMA1001627,	MAMMA1001633,	MAMMA1001743,	MAMMA1001820,	MAMMA1001837,
	MAMMA1002617,	MAMMA1002650,	MAMMA1002937,	NT2RM1000055,	NT2RM1000086,	NT2RM1000746,
45	NT2RM1000885,	NT2RM1000894,	NT2RM1001092,	NT2RM2000013,	NT2RM2000452,	NT2RM2000735,
	NT2RM2000740,	NT2RM2001035,	NT2RM2001105,	NT2RM2001575,	NT2RM2001670,	NT2RM2001716,
	NT2RM2001771,	NT2RM2002091,	NT2RM4000024,	NT2RM4000046,	NT2RM4000104,	NT2RM4000202,
	NT2RM4000531, NT2RM4000595, NT2RM4000733, NT2RM4000734,					
	NT2RM4000741,	NT2RM4000751,	NT2RM4000996,	NT2RM4001092,	NT2RM4001140,	NT2RM4001200,
50	NT2RM4001483,	NT2RM4001592,	NT2RM4001783,	NT2RM4001823,	NT2RM4001828,	NT2RM4001858,
	NT2RM4001979,	NT2RM4002066,	NT2RP1000086,	NT2RP1000111,	NT2RP1000574,	NT2RP1000902,
	NT2RP1001013,	NT2RP2000008,	NT2RP2000126,	NT2RP2000297,	NT2RP2000420,	NT2RP2001174,
	NT2RP2001233,	NT2RP2001756,	NT2RP2001869,	NT2RP2002046,	NT2RP2002252,	NT2RP2002270,
	NT2RP2002464,	NT2RP2002503,	NT2RP2002520,	NT2RP2002591,	NT2RP2002880,	NT2RP2002939,
55	NT2RP2002993,	NT2RP2003243,	NT2RP2003329,	NT2RP2003347,	NT2RP2003480,	NT2RP2003522,
	NT2RP2003564,	NT2RP2003714,	NT2RP2004013,	NT2RP2004066,	NT2RP2004187,	NT2RP2004920,
	NT2RP2004961,	NT2RP2005003,	NT2RP2005139,	NT2RP2005325,	NT2RP2005496,	NT2RP2005701,
	NT2RP2005722,	NT2RP2005776,	NT2RP2005942,	NT2RP2006238,	NT2RP2006436,	NT2RP3000050,

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	NT2RP3000320,	NT2RP3000512,	NT2RP3000527,	NT2RP3000590,	NT2RP3000603,	NT2RP3000605,
	NT2RP3000632,	NT2RP3001057,	NT2RP3001107,	NT2RP3001111,	NT2RP3001120,	NT2RP3001150,
	NT2RP3001268,	NT2RP3001338,	NT2RP3001398,	NT2RP3001527,	NT2RP3001688,	NT2RP3001855,
	NT2RP3002165,	NT2RP3002399,	NT2RP3002876,	NT2RP3003133,	NT2RP3003193,	NT2RP3003251,
5	NT2RP3003313,	NT2RP3003327,	NT2RP3003555,	NT2RP3004016,	NT2RP3004125,	NT2RP3004242,
	NT2RP3004428,	NT2RP3004498,	NT2RP3004566,	NT2RP3004617,	NT2RP4000210,	NT2RP4000398,
	NT2RP4000455,	NT2RP4000648,	NT2RP4000837,	NT2RP4000865,	NT2RP4000997,	NT2RP4001029,
	NT2RP4001080,	NT2RP4001213,	NT2RP4001433,	NT2RP4001529,	NT2RP4001551,	NT2RP4001568,
	NT2RP4001638,	NT2RP4001753,	NT2RP4001760,	NT2RP4001790,	NT2RP4001838,	NT2RP4001938,
10	NT2RP4002078,	NT2RP4002081,	NT2RP5003461,	OVARC1000151,	OVARC1000241,	OVARC1000479,
	OVARC1001271,	OVARC1001417,	OVARC1001436,	PLACE1000133,	PLACE1000583,	PLACE1000706,
	PLACE1000786,	PLACE1000979,	PLACE1001118,	PLACE1001238,	PLACE1001294,	PLACE1001304,
	PLACE1001383,	PLACE1001602,	PLACE1001632,	PLACE1002171,	PLACE1002438,	PLACE1002450,
	PLACE1002532,	PLACE1002775,	PLACE1002834,	PLACE1003302,	PLACE1003605,	PLACE1003738,
15	PLACE1003885,	PLACE1004471,	PLACE1005584,	PLACE1005803,	PLACE1005966,	PLACE1006167,
	PLACE1006318,	PLACE1006438,	PLACE1006482,	PLACE1007239,	PLACE1007346,	PLACE1007488,
	PLACE1007547,	PLACE1007598,	PLACE1007955,	PLACE1008132,	PLACE1008201,	PLACE1009099,
	PLACE1009246,	PLACE1009308,	PLACE1009398,	PLACE1009798,	PLACE1010134,	PLACE1010702,
	PLACE1010771,	PLACE1010870,	PLACE1011160,	PLACE1011433,	PLACE1011576,	PLACE3000009,
20	PLACE3000169,	PLACE3000254,	PLACE4000128,	PLACE4000156,	PLACE4000192,	PLACE4000211,
	PLACE4000261,	PLACE4000450,	PLACE4000489,	THYRO1000085,	THYRO1000121,	THYRO1000242,
	THYRO1000488,	THYRO1000501,	THYRO1000569,	THYRO 1001100,	THYRO1001189,	THYRO1001809,
	Y79AA1000013,	Y79AA1000033,	Y79AA1000037,	Y79AA1000342,	Y79AA1000627,	Y79AA1000705,
	Y79AA1001299,	Y79AA1001312,	Y79AA1001391,	Y79AA1001533,	Y79AA1001613,	Y79AA1001866,
25	Y79AA1002103,	Y79AA1002229,	Y79AA1002433,	Y79AA1002472,	Y79AA1002482,	
[0279] The following 392 clones are categorized into disease-associated proteins.						
	HEMBA1000020,	HEMBA1000216,	HEMBA1000304,	HEMBA1000561,	HEMBA1000569,	HEMBA1000910,
	HEMBA1001043,	HEMBA1001059,	HEMBA1001071,	HEMBA1001088,	HEMBA1001569,	HEMBA1001661,
	HEMBA1001672,	HEMBA1001819,	HEMBA1001921,	HEMBA1002267,	HEMBA1002419,	HEMBA1002469,
30	HEMBA1002547,	HEMBA1002555,	HEMBA1002810,	HEMBA1002939,	HEMBA1002997,	HEMBA1003148,
	HEMBA1003369,	HEMBA1003417,	HEMBA1003418,	HEMBA1003433,	HEMBA1003538,	HEMBA1003555,
	HEMBA1003568,	HEMBA1003569,	HEMBA1003581,	HEMBA1004168,	HEMBA1004202,	HEMBA1004248,
	HEMBA1004275,	HEMBA1004321,	HEMBA1004353,	HEMBA1004356,	HEMBA1004479,	HEMBA1004509,
	HEMBA1004669,	HEMBA1005009,	HEMBA1005338,	HEMBA1005367,	HEMBA1005423,	HEMBA1005528,
35	HEMBA1005581,	HEMBA1005621,	HEMBA1005699,	HEMBA1006507,	HEMBA1006650,	HEMBA1006652,
	HEMBA1006737,	HEMBA1006807,	HEMBA1006877,	HEMBA1007121,	HEMBA1007243,	HEMBA1007243,
	HEMBA100693,	HEMBA1000927,	HEMBA1000985,	HEMBA1001068,	HEMBA1001282,	HEMBA1001339,
	HEMBA1001482,	HEMBA1001564,	HEMBA1001802,	HEMBA1001905,	HEMBA1001908,	HEMBA1002217,
	HEMBA1002477,	MAMMA1000388,	MAMMA1000731,	MAMMA1001305,	MAMMA1001633,	MAMMA1001868,
40	MAMMA1002170,	MAMMA1002198,	MAMMA1002268,	MAMMA1002485,	MAMMA1002530,	MAMMA1002858,
	MAMMA1002869,	MAMMA1002881,	MAMMA1003047,	MAMMA1003146,	MAMMA1003166,	NT2RM1000001,
	NT2RM1000153,	NT2RM1000252,	NT2RM1000555,	NT2RM1000770,	NT2RM1000826,	NT2RM1000850,
	NT2RM1001003,	NT2RM1001092,	NT2RM1001102,	NT2RM2000191,		
	NT2RM2000363,	NT2RM2000594,	NT2RM2000624,	NT2RM2000714,	NT2RM2000821,	NT2RM2001035,
45	NT2RM2001575,	NT2RM2001652,	NT2RM2001664,	NT2RM2001668,	NT2RM2001698,	NT2RM2001803,
	NT2RM2001839,	NT2RM4000155,	NT2RM4000471,	NT2RM4000486,	NT2RM4000657,	NT2RM4000751,
	NT2RM4000996,	NT2RM4001629,	NT2RM4001810,	NT2RM4001819,	NT2RM4001865,	NT2RM4001876,
	NT2RM4001940,	NT2RM4002066,	NT2RM4002093,	NT2RM4002146,	NT2RM4002161,	NT2RM4002323,
	NT2RM4002558,	NT2RM4002571,	NT2RP1000086,	NT2RP1000574,	NT2RP1000738,	NT2RP1000825,
50	NT2RP1000833,	NT2RP1000959,	NT2RP1000966,	NT2RP1001013,	NT2RP1001185,	NT2RP1001482,
	NT2RP1001665,	NT2RP2000070,	NT2RP2000147,	NT2RP2000224,	NT2RP2000248,	NT2RP2000297,
	NT2RP2000310,	NT2RP2000414,	NT2RP2000420,	NT2RP2000523,	NT2RP2000809,	NT2RP2000812,
	NT2RP2001233,	NT2RP2001327,	NT2RP2001378,	NT2RP2001394,	NT2RP2001397,	NT2RP2001460,
	NT2RP2001520,	NT2RP2001536,	NT2RP2001876,	NT2RP2001898,	NT2RP2002025,	NT2RP2002058,
55	NT2RP2002124,	NT2RP2002325,	NT2RP2002503,	NT2RP2002959,	NT2RP2003000,	NT2RP2003157,
	NT2RP2003164,	NT2RP2003228,	NT2RP2003295,	NT2RP2003517,	NT2RP2003564,	NT2RP2003604,
	NT2RP2003714,	NT2RP2003737,	NT2RP2003952,	NT2RP2004013,	NT2RP2004170,	NT2RP2004587,
	NT2RP2004732,	NT2RP2004933,	NT2RP2005003,	NT2RP2005144,	NT2RP2005239,	NT2RP2005276,

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NT2RP2005288, NT2RP2005315, NT2RP2005325, NT2RP2005336, NT2RP2005358, NT2RP2005407,
 NT2RP2005436, NT2RP2005476, NT2RP2005525, NT2RP2005694, NT2RP2005719, NT2RP2006043,
 NT2RP2006071, NT2RP2006219, NT2RP2006312, NT2RP2006456, NT2RP3000050, NT2RP3000068,
 NT2RP3000085, NT2RP3000299, NT2RP3000403, NT2RP3000596, NT2RP3000739, NT2RP3000753,
 5 NT2RP3000875, NT2RP3001057, NT2RP3001081, NT2RP3001216, NT2RP3001307, NT2RP3001338,
 NT2RP3001427, NT2RP3001428, NT2RP3001679, NT2RP3001723, NT2RP3001855, NT2RP3001898,
 NT2RP3001969, NT2RP3002056, NT2RP3002062, NT2RP3002151, NT2RP3002351, NT2RP3002399,
 NT2RP3002953, NT2RP3002988, NT2RP3003078, NT2RP3003251, NT2RP3003282, NT2RP3003313,
 NT2RP3003327, NT2RP3003409, NT2RP3003672, NT2RP3003831, NT2RP3004016, NT2RP3004078,
 10 NT2RP3004209, NT2RP3004258, NT2RP3004490, NT2RP3004534, NT2RP3004569, NT2RP3004572,
 NT2RP4000109, NT2RP4000367, NT2RP4000376, NT2RP4000449, NT2RP4000855, NT2RP4000879,
 NT2RP4000925, NT2RP4001086, NT2RP4001126, NT2RP4001150, NT2RP4001213, NT2RP4001276,
 NT2RP4001407, NT2RP4001433, NT2RP4001483, NT2RP4001575, NT2RP4001760, NT2RP4001861,
 NT2RP4002078, NT2RP4002791, OVARC1000014, OVARC1000139, OVARC1000520, OVARC1000722,
 15 OVARC1000771, OVARC1000834, OVARC1001051, OVARC1001113, OVARC1001244, OVARC1001372,
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 35 **[0280]** Among them, Swiss-Prot database search and GenBank or UniGene database search revealed that the fol-
 lowing 380 clones matched the data of genes or proteins which had been registered in the database of Online Mendelian
 Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/Omim/>), which is a database of human genes and diseases.
 (The corresponding OMIM numbers are parenthetically indicated following the clone names.)
 40 HEMBB1000985(147485), HEMBB1001068(603142), HEMBB1001282(182900), HEMBB1001339(300080),
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	NT2RP2003295(603494),	NT2RP2003517(190040),	NT2RP2003564(109092),	NT2RP2003604(604785),
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30	NT2RP4002078(603971),	NT2RP4002791(189940),	OVARC1000014(603371),	OVARC1000139(603486),
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35	PLACE1000420(600312),	PLACE1000583(194558),	PLACE1000588(600411),	PLACE1001171(310400),
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50	PLACE2000072(603430),	PLACE2000216(182790),	PLACE2000399(313470),	PLACE2000438(602273),
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55	THYRO1000934(179035),	THYRO1001120(602582),	THYRO1001189(603971),	THYRO1001204(603169),
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Y79AA1001874(600315), Y79AA1002204(605033), Y79AA1002210(191161), Y79AA1002472(603971),
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[0281] The following 425 clones presumably belong to enzymes and/or metabolism-associated proteins.

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	HEMBA1003179,	HEMBA1003250,	HEMBA1003291,	HEMBA1003408,	HEMBA1003538,	HEMBA1003679,
	HEMBA1003680,	HEMBA1004199,	HEMBA1004227,	HEMBA1004408,	HEMBA1004509,	HEMBA1004734,
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	NT2RM2000951,	NT2RM2001238,	NT2RM2001547,	NT2RM2001632,	NT2RM2001664,	NT2RM2001698,
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	OVARC1001942,	OVARC1002156,	OVARC1002165,	PLACE1000007,	PLACE1000142,	PLACE1000185,
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	PLACE1002991,	PLACE1003174,	PLACE1003176,	PLACE1003709,	PLACE1003885,	PLACE1003888,
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 THYRO1000605, THYRO1000662, THYRO1000756, THYRO1000852, THYRO1000926, THYRO 1000934,
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 15 Y79AA1001394, Y79AA1001493, Y79AA1001548, Y79AA1001581, Y79AA1001603, Y79AA1001827,
 Y79AA1002027, Y79AA1002209, Y79AA1002211, Y79AA1002361, Y79AA1002416,

[0282] The following 217 clones presumably belong to a group of cDNAs encoding ATP- and/or GTP-binding proteins.

HEMBA1000012, HEMBA1000129, HEMBA1000185, HEMBA1000491, HEMBA1000531, HEMBA1001019,
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 25 MAMMA1001768, MAMMA1003127, NT2RM1000187, NT2RM1000388, NT2RM1000702, NT2RM1000772,
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 NT2RM2001345, NT2RM2001823, NT2RM2002128, NT2RM4000155, NT2RM4000191, NT2RM4000356,
 NT2RM4000496, NT2RM4000611, NT2RM4000733, NT2RM4000820, NT2RM4001084, NT2RM4001178,
 NT2RM4001344, NT2RM4001444, NT2RM4001592, NT2RM4001714, NT2RM4001758, NT2RM4001880,
 30 NT2RM4002062, NT2RM4002174, NT2RM4002205, NT2RM4002527, NT2RM4002594, NT2RM4002623,
 NT2RP1000470, NT2RP1000478, NT2RP1000915, NT2RP1000958, NT2RP1001080, NT2RP1001410,
 NT2RP1001569, NT2RP2000126, NT2RP2000258, NT2RP2000329, NT2RP2000660, NT2RP2000668,
 NT2RP2000710, NT2RP2000812, NT2RP2000880, NT2RP2001245, NT2RP2001392, NT2RP2002606,
 NT2RP2003277, NT2RP2003912, NT2RP2004538, NT2RP2004568,
 35 NT2RP2004689, NT2RP2004768, NT2RP2004791, NT2RP2004920, NT2RP2005344, NT2RP2005393,
 NT2RP2005763, NT2RP2006534, NT2RP3000046, NT2RP3000252, NT2RP3000350, NT2RP3000359,
 NT2RP3000366, NT2RP3000397, NT2RP3000759, NT2RP3000845, NT2RP3000875, NT2RP3001150,
 NT2RP3001427, NT2RP3001453, NT2RP3001529, NT2RP3001730, NT2RP3001799, NT2RP3001857,
 NT2RP3001938, NT2RP3002007, NT2RP3002151, NT2RP3002330, NT2RP3002399, NT2RP3002671,
 40 NT2RP3003301, NT2RP3003353, NT2RP3003589, NT2RP3003809, NT2RP3003876, NT2RP3004189,
 NT2RP3004428, NT2RP3004578, NT2RP4000290, NT2RP4000481, NT2RP4000518, NT2RP4000781,
 NT2RP4000839, NT2RP4000929, NT2RP4001041, NT2RP4001079, NT2RP4001375, NT2RP4001414,
 NT2RP4001592, NT2RP4001634, NT2RP4001644, NT2RP4001656, NT2RP4001896, NT2RP4002047,
 NT2RP4002058, NT2RP4002408, NT2RP5003477, OVARC1000013, OVARC1000304, OVARC1000556,
 45 OVARC1000771, OVARC1000800, OVARC1001068, OVARC1002138, PLACE1000040, PLACE1000588,
 PLACE1001104, PLACE1001739, PLACE1002433, PLACE1002437, PLACE1002714, PLACE1003394,
 PLACE1003521, PLACE1003915, PLACE1004902, PLACE1005243, PLACE1005305, PLACE1005549,
 PLACE1005739, PLACE1005921, PLACE1006119, PLACE1006196, PLACE1006552, PLACE1006956,
 PLACE1007409, PLACE1007697, PLACE1007946, PLACE1008244, PLACE1009404, PLACE1009476,
 50 PLACE1009596, PLACE1009908, PLACE1010134, PLACE1010720, PLACE1010896, PLACE1011109,
 PLACE1011114, PLACE1011310, PLACE1011922, PLACE2000014, PLACE2000039, PLACE2000274,
 PLACE2000404, PLACE2000427, PLACE3000350, PLACE4000009, PLACE4000014, PLACE4000326,
 SKNMC1000013, THYRO1000072, THYRO1001458, Y79AA1000833, Y79AA1000962, Y79AA1001394,
 Y79AA1001875, Y79AA1001963, Y79AA1002209,

[0283] The following 320 clones presumably belong to nuclear proteins.

HEMBA1000005, HEMBA1000158, HEMBA1000216, HEMBA1000561, HEMBA1000591, HEMBA1001088,
 HEMBA1001137, HEMBA1001405, HEMBA1001510, HEMBA1001579, HEMBA1001809, HEMBA1001819,
 HEMBA1001824, HEMBA1001847, HEMBA1001869, HEMBA1002177, HEMBA1002241, HEMBA1002495,

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	HEMBA1002569,	HEMBA1002935,	HEMBA1002951,	HEMBA1002999,	HEMBA1003408,	HEMBA1003545,
	HEMBA1003662,	HEMBA1003684,	HEMBA1003690,	HEMBA1003760,	HEMBA1004203,	HEMBA1004321,
	HEMBA1004353,	HEMBA1004479,	HEMBA1004973,	HEMBA1005219,	HEMBA1005359,	HEMBA1005558,
	HEMBA1005931,	HEMBA1006278,	HEMBA1006283,	HEMBA1006359,	HEMBA1006485,	HEMBA1007087,
5	HEMBA1000226,	HEMBA1000789,	HEMBA1001011,	HEMBA1001056,	HEMBA1001242,	HEMBA1001482,
	HEMBA1001915,	HEMBA1002134,	HEMBA1002217,	MAMMA1000183,	MAMMA1000731,	MAMMA1001105,
	MAMMA1001222,	MAMMA1001260,	MAMMA1001633,	MAMMA1001743,	MAMMA1001837,	MAMMA1002617,
	MAMMA1002869,	MAMMA1002937,	MAMMA1003011,	NT2RM1000086,	NT2RM1000187,	NT2RM1000666,
	NT2RM1000885,	NT2RM1000894,	NT2RM1001059,	NT2RM1001092,	NT2RM2000013,	NT2RM2000588,
10	NT2RM2000624,	NT2RM2000735,	NT2RM2000740,	NT2RM2001105,	NT2RM2001635,	NT2RM2001670,
	NT2RM2001771,	NT2RM2001823,	NT2RM2001936,	NT2RM2001989,	NT2RM2002004,	NT2RM2002088,
	NT2RM2002091,	NT2RM4000024,	NT2RM4000046,	NT2RM4000104,	NT2RM4000202,	NT2RM4000215,
	NT2RM4000290,	NT2RM4000531,	NT2RM4000751,	NT2RM4000996,	NT2RM4001092,	NT2RM4001140,
	NT2RM4001200,	NT2RM4001483,	NT2RM4001566,	NT2RM4001592,		
15	NT2RM4001597,	NT2RM4001783,	NT2RM4001823,	NT2RM4001828,	NT2RM4001858,	NT2RM4001979,
	NT2RP1000035,	NT2RP1000111,	NT2RP1000493,	NT2RP1000574,	NT2RP1000630,	NT2RP1000902,
	NT2RP1000915,	NT2RP1000958,	NT2RP1000966,	NT2RP1001013,	NT2RP1001177,	NT2RP2000008,
	NT2RP2000076,	NT2RP2000126,	NT2RP2000153,	NT2RP2000161,	NT2RP2000248,	NT2RP2000258,
	NT2RP2000297,	NT2RP2000420,	NT2RP2000931,	NT2RP2001233,	NT2RP2001420,	NT2RP2001756,
20	NT2RP2001869,	NT2RP2002079,	NT2RP2002270,	NT2RP2002503,	NT2RP2002591,	NT2RP2002880,
	NT2RP2002939,	NT2RP2002993,	NT2RP2003137,	NT2RP2003157,	NT2RP2003277,	NT2RP2003286,
	NT2RP2003308,	NT2RP2003347,	NT2RP2003714,	NT2RP2003912,	NT2RP2004013,	NT2RP2004187,
	NT2RP2004689,	NT2RP2004920,	NT2RP2005393,	NT2RP2005436,	NT2RP2005496,	NT2RP2005539,
	NT2RP2005701,	NT2RP2005767,	NT2RP2005776,	NT2RP2005933,	NT2RP2005942,	NT2RP2006043,
25	NT2RP2006436,	NT2RP3000031,	NT2RP3000050,	NT2RP3000397,	NT2RP3000512,	NT2RP3000527,
	NT2RP3000590,	NT2RP3000603,	NT2RP3000632,	NT2RP3000917,	NT2RP3001057,	NT2RP3001107,
	NT2RP3001120,	NT2RP3001253,	NT2RP3001338,	NT2RP3001384,	NT2RP3001398,	NT2RP3001427,
	NT2RP3001428,	NT2RP3001472,	NT2RP3001646,	NT2RP3001671,	NT2RP3001792,	NT2RP3001855,
	NT2RP3002056,	NT2RP3002165,	NT2RP3002399,	NT2RP3002876,	NT2RP3003193,	NT2RP3003212,
30	NT2RP3003555,	NT2RP3004016,	NT2RP3004206,	NT2RP3004424,	NT2RP3004428,	NT2RP3004566,
	NT2RP3004617,	NT2RP4000078,	NT2RP4000111,	NT2RP4000210,	NT2RP4000398,	NT2RP4000481,
	NT2RP4000518,	NT2RP4000997,	NT2RP4001148,	NT2RP4001206,	NT2RP4001213,	NT2RP4001433,
	NT2RP4001568,	NT2RP4001638,	NT2RP4001696,	NT2RP4001753,	NT2RP4001938,	NT2RP4002058,
	NT2RP4002078,	NT2RP4002081,	NT2RP4002791,	OVARC1000006,	OVARC1000087,	OVARC1000091,
35	OVARC1000241,	OVARC1000326,	OVARC1000556,	OVARC1000846,	OVARC1001038,	OVARC1001180,
	OVARC1001232,	OVARC1001271,	OVARC1001306,	OVARC1001436,	OVARC1002112,	PLACE1000133,
	PLACE1000184,	PLACE1000406,	PLACE1000583,	PLACE1000596,	PLACE1000979,	PLACE1001118,
	PLACE1001383,	PLACE1001632,	PLACE1002171,	PLACE1002433,	PLACE1002438,	PLACE1002532,
	PLACE1002775,	PLACE1002816,	PLACE1002834,	PLACE1003100,	PLACE1003190,	PLACE1003302,
40	PLACE1003519,	PLACE1003521,	PLACE1003605,	PLACE1003704,	PLACE1003738,	PLACE1003885,
	PLACE1003923,	PLACE1004302,	PLACE1004471,	PLACE1004564,	PLACE1004814,	PLACE1004902,
	PLACE1005287,	PLACE1005876,	PLACE1005966,	PLACE1006167,	PLACE1006438,	PLACE1006482,
	PLACE1006829,	PLACE1006878,	PLACE1006917,	PLACE1007014,	PLACE1007547,	PLACE1007598,
	PLACE1007688,	PLACE1007969,	PLACE1008044,	PLACE1008132,	PLACE1008603,	PLACE1009099,
45	PLACE1009130,	PLACE1009308,	PLACE1009398,	PLACE1010134,	PLACE1010194,	PLACE1010702,
	PLACE1010720,	PLACE1010870,	PLACE1011056,	PLACE1011433,	PLACE1011664,	PLACE2000014,
	PLACE2000427,	PLACE3000009,	PLACE3000169,	PLACE4000014,	PLACE4000156,	PLACE4000192,
	PLACE4000261,	PLACE4000326,	PLACE4000489,	SKNMC1000011,	THYRO1000085,	THYRO1000242,
	THYRO1000585,	THYRO1001100,	THYRO1001189,	THYRO1001809,	Y79AA1000037,	Y79AA1000214,
50	Y79AA1000231,	Y79AA1000589,	Y79AA1000752,	Y79AA1001391,	Y79AA1001613,	Y79AA1001705,
	Y79AA1001963,	Y79AA1002431,	Y79AA1002472,	Y79AA1002482		

[0284] The following 292 clones presumably belong to DNA- and/or RNA-binding proteins.

	HEMBA1000158,	HEMBA1000216,	HEMBA1000561,	HEMBA1000591,	HEMBA1000851,	HEMBA1001088,
	HEMBA1001137,	HEMBA1001405,	HEMBA1001510,	HEMBA1001804,	HEMBA1001809,	HEMBA1001819,
55	HEMBA1001847,	HEMBA1001869,	HEMBA1002177,	HEMBA1002935,	HEMBA1003408,	HEMBA1003545,
	HEMBA1003568,	HEMBA1003591,	HEMBA1003662,	HEMBA1003684,	HEMBA1003760,	HEMBA1003783,
	HEMBA1003805,	HEMBA1003953,	HEMBA1004321,	HEMBA1004354,	HEMBA1004389,	HEMBA1004479,
	HEMBA1004669,	HEMBA1004847,	HEMBA1004973,	HEMBA1005202,	HEMBA1005359,	HEMBA1005931,

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HEMBA1006248, HEMBA1006278, HEMBA1006283, HEMBA1006359, HEMBA1006652, HEMBA1007087,
HEMBA1007194, HEMBB1000264, HEMBB1000789, HEMBB1001011, HEMBB1001482, HEMBB1001736,
HEMBB1001749, HEMBB1001839, HEMBB1002217, MAMMA1000183, MAMMA1000284, MAMMA1000731,
5 MAMMA1001105, MAMMA1001222, MAMMA1001260, MAMMA1001743, MAMMA1001837, MAMMA1002385,
MAMMA1002617, MAMMA1002869, MAMMA1002937, MAMMA1003011, NT2RM1000086, NT2RM1000539,
NT2RM1000555, NT2RM1000666, NT2RM1000691, NT2RM1000826, NT2RM1000885, NT2RM1001059,
NT2RM1001092, NT2RM2000371, NT2RM2000624, NT2RM2000735, NT2RM2001105, NT2RM2001424,
NT2RM2001575, NT2RM2001605, NT2RM2001670, NT2RM2001771, NT2RM2001823, NT2RM2001989,
10 NT2RM2002004, NT2RM2002014, NT2RM2002088, NT2RM2002091, NT2RM4000046, NT2RM4000104,
NT2RM4000167, NT2RM4000191, NT2RM4000202, NT2RM4000531, NT2RM4000595, NT2RM4000733,
NT2RM4000751, NT2RM4000996, NT2RM4001092, NT2RM4001140,
NT2RM4001178, NT2RM4001200, NT2RM4001483, NT2RM4001592, NT2RM4001783, NT2RM4001823,
NT2RM4001828, NT2RM4001858, NT2RM4001880, NT2RM4001979, NT2RM4002093, NT2RM4002109,
15 NT2RP1000470, NT2RP1000493, NT2RP1000574, NT2RP1000902, NT2RP1000966, NT2RP1001013,
NT2RP1001073, NT2RP1001080, NT2RP2000008, NT2RP2000153, NT2RP2000258, NT2RP2000297,
NT2RP2001127, NT2RP2001174, NT2RP2001233, NT2RP2001511, NT2RP2001756, NT2RP2001869,
NT2RP2002079, NT2RP2002099, NT2RP2002503, NT2RP2002591, NT2RP2002939, NT2RP2003157,
NT2RP2003329, NT2RP2003347, NT2RP2003480, NT2RP2003522, NT2RP2003564, NT2RP2003714,
20 NT2RP2004187, NT2RP2004568, NT2RP2004920, NT2RP2005003, NT2RP2005139, NT2RP2005168,
NT2RP2005436, NT2RP2005496, NT2RP2005701, NT2RP2005763, NT2RP2005776, NT2RP2005942,
NT2RP2006043, NT2RP2006436, NT2RP2006464, NT2RP3000050, NT2RP3000512, NT2RP3000527,
NT2RP3000562, NT2RP3000590, NT2RP3000603, NT2RP3000624, NT2RP3000632, NT2RP3000994,
NT2RP3001057, NT2RP3001107, NT2RP3001120, NT2RP3001150, NT2RP3001155, NT2RP3001338,
NT2RP3001398, NT2RP3001472, NT2RP3001672, NT2RP3001688, NT2RP3001724, NT2RP3001792,
25 NT2RP3001855, NT2RP3002165, NT2RP3002399, NT2RP3002876, NT2RP3003138, NT2RP3003193,
NT2RP3003251, NT2RP3003327, NT2RP3003555, NT2RP3004013, NT2RP3004078, NT2RP3004428,
NT2RP3004490, NT2RP3004566, NT2RP3004594, NT2RP3004617, NT2RP3004618, NT2RP4000111,
NT2RP4000398, NT2RP4000455, NT2RP4000518, NT2RP4000648, NT2RP4000865, NT2RP4000929,
NT2RP4001080, NT2RP4001095, NT2RP4001213, NT2RP4001433, NT2RP4001568, NT2RP4001696,
30 NT2RP4001753, NT2RP4001838, NT2RP4001938, NT2RP4002078, OVARC1000006, OVARC1000087,
OVARC1000241, OVARC1000746, OVARC1000846, OVARC1001232, OVARC1001271, OVARC1001306,
OVARC1001987, OVARC1002112, OVARC1000406, PLACE1000583, PLACE1000979, PLACE1001118,
PLACE1001632, PLACE1001739, PLACE1002438, PLACE1002532, PLACE1002775, PLACE1002834,
35 PLACE1003302, PLACE1003519, PLACE1003605, PLACE1003704, PLACE1003738, PLACE1003885,
PLACE1004471, PLACE1004564, PLACE1004814, PLACE1005584, PLACE1005876, PLACE1005951,
PLACE1006196, PLACE1006482, PLACE1006488, PLACE1006531, PLACE1006917, PLACE1007346,
PLACE1007547, PLACE1007598, PLACE1007688, PLACE1007969, PLACE1008132, PLACE1009099,
PLACE1009246, PLACE1009398, PLACE1009476, PLACE1009622, PLACE1010053, PLACE1010194,
PLACE1010702, PLACE1010870, PLACE1011056, PLACE1011114, PLACE1011433, PLACE2000427,
40 PLACE3000009, PLACE3000169, PLACE4000014, PLACE4000156, PLACE4000192, PLACE4000261,
PLACE4000489, SKNMC1000091, THYRO1000085, THYRO1000242, THYRO1000501, THYRO1001100,
THYRO1001189, THYRO1001809, Y79AA1000037, Y79AA1000349, Y79AA1000752, Y79AA1001211,
Y79AA1001312, Y79AA1001391, Y79AA1001613, Y79AA1002103, Y79AA1002472, Y79AA1002482,
[0285] The following 66 clones presumably belong to the category of RNA synthesis-associated proteins.
45 HEMBA1000591, HEMBA1001579, HEMBA1003179, HEMBA1003591, HEMBA1006278, HEMBB1000226,
NT2RM1000187, NT2RM1000852, NT2RM2000624, NT2RM2001989, NT2RM2002100, NT2RM4000191,
NT2RM4001178, NT2RM4002093, NT2RP1000035, NT2RP1000272, NT2RP1000470, NT2RP1001080,
NT2RP2000153, NT2RP2002928, NT2RP2003157, NT2RP2004568, NT2RP2005126, NT2RP2005436,
NT2RP2005539, NT2RP2005605, NT2RP2005776, NT2RP2005942, NT2RP2006043, NT2RP2006238,
50 NT2RP3000361, NT2RP3000397, NT2RP3001671, NT2RP3004504, NT2RP4000078, NT2RP4000111,
NT2RP4000481, NT2RP4000518, NT2RP4000614, NT2RP4000929, NT2RP4001696, NT2RP4002058,
OVARC1001232, OVARC1001577, OVARC1000406, PLACE1000596, PLACE1000755, PLACE1001739,
PLACE1003704, PLACE1003885, PLACE1004564, PLACE1004814, PLACE1004902, PLACE1005373,
PLACE1005646, PLACE1005876, PLACE1006196, PLACE1006626, PLACE1006878, PLACE1006917,
55 PLACE1009476, PLACE1009925, PLACE1010194, PLACE1011114, THYRO1000121, Y79AA1001963,
[0286] The following 183 clones presumably belong to protein synthesis-associated and/or protein transport-associated proteins.
HEMBA1000012, HEMBA1000141, HEMBA1000592, HEMBA1003617, HEMBA1003773, HEMBA1004202,

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HEMBA1004276, HEMBA1004734, HEMBA1004847, HEMBA1004929, HEMBA1004930, HEMBA1005047,
HEMBA1005202, HEMBA1006031, HEMBA1006272, HEMBA1006474, HEMBA1006652, HEMBA1006914,
HEMBA1006973, HEMBA1007224, HEMBB1000915, HEMBB1001112, HEMBB1001137, HEMBB1001736,
HEMBA1001831, HEMBB1001915, MAMMA1000085, MAMMA1000734, MAMMA1001008, MAMMA1002170,
5 MAMMA1002219, MAMMA1002236, MAMMA1002619, NT2RM1000661, NT2RM1000833, NT2RM2000092,
NT2RM2000504, NT2RM2000577, NT2RM2000821, NT2RM2001201, NT2RM2001592, NT2RM2001613,
NT2RM2001648, NT2RM2001730, NT2RM2001760, NT2RM2002055, NT2RM4000155, NT2RM4000169,
NT2RM4000344, NT2RM4000356, NT2RM4000421, NT2RM4000712, NT2RM4001054, NT2RM4001203,
NT2RM4001382, NT2RM4001444, NT2RM4002062, NT2RM4002205, NT2RM4002623, NT2RP1000326,
10 NT2RP1000522, NT2RP1000547, NT2RP1000746, NT2RP1000947, NT2RP1001569, NT2RP2000147,
NT2RP2000710, NT2RP2000880, NT2RP2000943, NT2RP2001290, NT2RP2001392, NT2RP2001601,
NT2RP2001613, NT2RP2001660, NT2RP2001740, NT2RP2002124, NT2RP2002606, NT2RP2002862,
NT2RP2002959, NT2RP2002980, NT2RP2003137, NT2RP2003158, NT2RP2003391, NT2RP2003394,
NT2RP2003401, NT2RP2003433, NT2RP2003704, NT2RP2003713, NT2RP2003737, NT2RP2003760,
15 NT2RP2003981, NT2RP2004366, NT2RP2004389, NT2RP2004791, NT2RP2005012, NT2RP2005116,
NT2RP2005360, NT2RP2005763, NT2RP2005784, NT2RP3000366,
NT2RP3000759, NT2RP3000968, NT2RP3001113, NT2RP3001690, NT2RP3002045, NT2RP3002151,
NT2RP3002529, NT2RP3002671, NT2RP3003301, NT2RP3003846, NT2RP3003876, NT2RP3004209,
NT2RP4000370, NT2RP4000457, NT2RP4000879, NT2RP4000927, NT2RP4001041, NT2RP4001117,
20 NT2RP4001313, NT2RP4001315, NT2RP4001574, NT2RP4001592, OVARC1000013, OVARC1000071,
OVARC1000085, OVARC1000465, OVARC1000564, OVARC1000771, OVARC1000862, OVARC1001171,
OVARC1001180, OVARC1001342, PLACE1000007, PLACE1000061, PLACE1000081, PLACE1000492,
PLACE1000863, PLACE1001092, PLACE1001748, PLACE1002090, PLACE1003174, PLACE1003915,
PLACE1004104, PLACE1004270, PLACE1004743, PLACE1005557, PLACE1005813, PLACE1006170,
25 PLACE1006488, PLACE1006829, PLACE1007706, PLACE1007729, PLACE1008273, PLACE1008402,
PLACE1008790, PLACE1008813, PLACE1009094, PLACE1009130, PLACE1009477, PLACE1009721,
PLACE1009845, PLACE1010074, PLACE1010547, PLACE1011109, PLACE1011229, PLACE1011477,
PLACE1012031, PLACE2000404, PLACE3000059, PLACE3000121, PLACE4000269, PLACE4000654,
SKNMC1000011, THYRO1000983, THYRO1001003, THYRO1001313, Y79AA1000560, Y79AA1000784,
30 Y79AA1000968, Y79AA1001493, Y79AA1001875, Y79AA1002027, Y79AA1002209,
[0287] The following 130 clones presumably belong to cytoskeletal-associated proteins.
HEMBA1000156, HEMBA1000168, HEMBA1000411, HEMBA1000588, HEMBA1001043, HEMBA1001651,
HEMBA1001661, HEMBA1002102, HEMBA1002161, HEMBA1002939, HEMBA1003235, HEMBA1003581,
HEMBA1004499, HEMBA1004534, HEMBA1004697, HEMBA1004929, HEMBA1004972, HEMBA1005582,
35 HEMBA1005595, HEMBA1006344, HEMBA1006737, HEMBB1001175, HEMBB1001282, HEMBB1001562,
HEMBA1001802, MAMMA1000824, MAMMA1001041, MAMMA1001576, MAMMA1001679, MAMMA1001735,
MAMMA1002297, MAMMA1002351, MAMMA1002622, MAMMA1002637, MAMMA1003127, NT2RM1000850,
NT2RM1000898, NT2RM2000030, NT2RM2000260, NT2RM2000691, NT2RM2001324, NT2RM4000169,
NT2RM4000229, NT2RM4000515, NT2RM4001217, NT2RP1000202, NT2RP1000348, NT2RP1000460,
40 NT2RP1000478, NT2RP1001033, NT2RP1001294, NT2RP1001302, NT2RP2000070, NT2RP2000812,
NT2RP2000814, NT2RP2001168, NT2RP2001245, NT2RP2001634, NT2RP2001900, NT2RP2003307,
NT2RP2003394, NT2RP2004041, NT2RP2004242, NT2RP2004538, NT2RP2004587, NT2RP2004681,
NT2RP2004732, NT2RP2004978, NT2RP2005491, NT2RP2005531, NT2RP2005712, NT2RP2006275,
NT2RP3000753, NT2RP3001113, NT2RP3001216, NT2RP3001239, NT2RP3001272, NT2RP3001554,
45 NT2RP3001690, NT2RP3001799, NT2RP3002688, NT2RP3003061, NT2RP3003185, NT2RP3003230,
NT2RP3004569, NT2RP3004578, NT2RP4001004, NT2RP4001086, NT2RP4001256, NT2RP4001567,
NT2RP4001927, OVARC1000001, OVARC1000106, OVARC1000437, OVARC1000520, OVARC1000679,
OVARC1001731, OVARC1002050, PLACE1001104, PLACE1002571,
PLACE1002591, PLACE1002655, PLACE1002714, PLACE1003625, PLACE1005287, PLACE1006552,
50 PLACE1007946, PLACE1008426, PLACE1010148, PLACE1010547, PLACE1010743, PLACE1010896,
PLACE1010960, PLACE1011310, PLACE1011922, PLACE2000216, PLACE2000274, PLACE2000371,
PLACE2000458, PLACE3000145, PLACE3000416, PLACE4000009, THYRO1000132, THYRO1001405,
THYRO1001458, Y79AA1000368, Y79AA1000794, Y79AA1000833, Y79AA1000962, Y79AA1002208,
[0288] The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated
55 proteins.
HEMBA1001019, HEMBA1001595, HEMBA1002363, HEMBA1002997, HEMBA1003136, HEMBA1003369,
HEMBA1004131, HEMBA1004354, HEMBA1005621, HEMBB1000037, HEMBB1000264, MAMMA1001768,
MAMMA1002769, NT2RM1000354, NT2RM1000430, NT2RM1000874, NT2RM2001256, NT2RM2001743,

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NT2RM2001896, NT2RM2002145, NT2RM4000215, NT2RM4001714, NT2RP1000163, NT2RP1000333,
NT2RP1000439, NT2RP2000346, NT2RP2001397, NT2RP2002595, NT2RP2003177, NT2RP2003596,
NT2RP2003912, NT2RP2004396, NT2RP2005037, NT2RP2005520, NT2RP2005669, NT2RP2005835,
NT2RP3001730, NT2RP3002081, NT2RP4000210, NT2RP4000415, NT2RP4001414, NT2RP4001634,
5 OVARC1000013, OVARC1000937, PLACE1001383, PLACE1002433, PLACE1004316, PLACE1005287,
PLACE1008808, PLACE1010720, PLACE1010833, Y79AA1000748, Y79AA1001236, Y79AA1001394,

[0289] The following 36 clones presumably belong to the category of embryogenesis- and/or development-associated proteins.

HEMBA1000518, HEMBA1001847, HEMBA1001869, HEMBA1003545, HEMBA1004973, HEMBB1002442,
10 MAMMA1001837, NT2RM2001670, NT2RM4000046, NT2RM4000531, NT2RM4001140, NT2RM4001858,
NT2RP2002078, NT2RP2004187, NT2RP2006436, NT2RP3000603, NT2RP3000994, NT2RP3001580,
NT2RP3001708, NT2RP3003071, NT2RP3004472, NT2RP3004617, NT2RP4000246, NT2RP4001567,
OVARC1000304, OVARC1000746, PLACE1000793, PLACE1002532, PLACE1003258, PLACE1003625,
PLACE1004460, PLACE1009622, PLACE4000558, THYRO1000085, Y79AA1001391, Y79AA1001692,

[0290] The following 30 clones presumably belong to cellular defense-associated proteins.

HEMBA1000005, HEMBA1000531, HEMBA1003417, HEMBA1006253, NT2RM4000354, NT2RM4001880,
NT2RP1000333, NT2RP1000493, NT2RP2000006, NT2RP2000045, NT2RP2000809, NT2RP2001536,
NT2RP2002464, NT2RP2004920, NT2RP2005037, NT2RP3000590, NT2RP3001426, NT2RP3002062,
NT2RP3002785, NT2RP3004262, NT2RP4001555, NT2RP4001638, PLACE1006958, PLACE1008275,
20 PLACE1009113, PLACE1011858, PLACE4000014, THYRO1000684, Y79AA1002139, Y79AA1002229,

[0291] Although it is unclear whether or not 261 clones out of clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using the full-length sequences thereof. The clone names and the gene definitions found in the result of homology search are shown below, separated with a double-slash mark, //.

25 HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds.

HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1

30 HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.

HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).

HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.

HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.

HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.

35 HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.

HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.

HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.

HEMBA1001744//SCY1 PROTEIN.

HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.

40 HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.

HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].

HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.

HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, complete cds.

HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.

45 HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.

HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1).

HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.

HEMBA1004573//Homo sapiens mRNA for HELG protein.

50 HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.

HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).

HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.

HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.

HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.

55 HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7) mRNA, complete cds.

HEMBA1005666//Homo sapiens mRNA for DIPB protein.

HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.

HEMBA1006268//Homo sapiens HQOO24c mRNA, complete cds.

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HEMBA1006398//Human L1 element L1.6 putative p150 gene, complete cds.
HEMBA1006445//Homo sapiens putative tumor suppressor NOEY2 mRNA, complete cds.
HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.
5 HEMBA1007251//Homo sapiens F-box protein FBX29 (FBX29) mRNA, partial cds. HEMBB1000036//Homo sapiens CGI-51 protein mRNA, complete cds.
HEMBB1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINAL GUANYLYL CYCLASE ACTIVATOR PROTEIN P24).
HEMBB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.
HEMBB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds
10 HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).
HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.
HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.
HEMBB1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.
HEMBB1002266//NEURONAL PROTEIN.
15 HEMBB1002510//GYP7 PROTEIN.
HEMBB1002705//Homo sapiens CGI-27 protein mRNA, complete cds.
MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TEST)].
MAMMA1000625//GYP7 PROTEIN.
MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.
20 MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.
MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.
MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.
MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.
MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.
25 MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.
MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27.
MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.
NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).
30 NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT).
NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds.
NT2RM1000421//RIBONUCLEASE INHIBITOR.
NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A.
35 NT2RM1000623//RIBONUCLEASE INHIBITOR.
NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
NT2RM2000502//Rattus norvegicus W3O7 mRNA, complete cds.
NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.
NT2RM2000718//Homo sapiens endocrine regulator mRNA, complete cds.
40 NT2RM2001065//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.
NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.
NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.
NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.
45 NT2RM4000030//LAS1 PROTEIN.
NT2RM4000139//R.norvegicus trg mRNA.
NT2RM4000156//H. sapiens HPBR11-7 gene.
NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).
50 NT2RM4001047//MO25 PROTEIN.
NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.
NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.
NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.
NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).
55 NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds.
NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds.
NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.
NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).

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NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.
 NT2RM4001969//R.norvegicus mRNA for IP63 protein.
 NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.
 NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).
 5 NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.
 NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.
 NT2RP1000363//R.norvegicus LL5 mRNA.
 NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.
 NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.
 10 NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.
 NT2RP1000860//Homo sapiens KLO4P mRNA, complete cds.
 NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).
 NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.
 NT2RP1001395//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.
 15 NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).
 NT2RP1001494//MALE STERILITY PROTEIN 2.
 NT2RP2000054//Homo sapiens putative ring zinc finger protein NY-REN-43 antigen mRNA, complete cds.
 NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
 NT2RP2000133//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.
 20 NT2RP2000157//MLO2 PROTEIN.
 NT2RP2000764//NIFS PROTEIN.
 NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.
 NT2RP2001839//SCY1 PROTEIN.
 NT2RP2001883//Homo sapiens CGI-01 protein mRNA, complete cds.
 25 NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.
 NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6TP1 alpha
 mRNA, complete cds.
 NT2RP2002185//Homo sapiens ubiquilin mRNA, complete cds.
 NT2RP2002442//HESA PROTEIN.
 30 NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.
 NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.
 NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.
 NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.
 NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.
 35 NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds.
 NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).
 NT2RP2003871//Homo sapiens transposon-derived Buster1 transposase-like protein gene, complete cds.
 NT2RP2004425//Mus musculus axotrophin mRNA, complete cds.
 NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA, complete cds.
 40 NT2RP2004710//Mus musculus formin binding protein 30 mRNA, complete cds.
 NT2RP2004816//H58 PROTEIN.
 NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds.
 NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds.
 NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.
 45 NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).
 NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.
 NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
 NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds.
 NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.
 50 NT2RP3000047//NPL4 PROTEIN.
 NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).
 NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete
 cds.
 NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.
 55 NT2RP3001399//SSU72 PROTEIN.
 NT2RP3001407//SCY1 PROTEIN.
 NT2RP3001457//Drosophila melanogaster Melted (melt) mRNA, partial cds.
 NT2RP3001587//Human anthracycline-associated resistance ARX mRNA, complete cds.

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NT2RP3001712//Homo sapiens HP1-BP74 protein mRNA, complete cds.
 NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).
 NT2RP3001854//Homo sapiens novel retinal pigment epithelial cell protein (NORPEG) mRNA, complete cds.
 NT2RP3001931//Rattus norvegicus clone C48 CDK5 activator-binding protein mRNA, complete cds.
 5 NT2RP3002273//SCD6 PROTEIN.
 NT2RP3002631//Homo sapiens Ran binding protein 11 mRNA, complete cds.
 NT2RP3002682//Homo sapiens CGI-145 protein mRNA, complete cds.
 NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.
 NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.
 10 NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).
 NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds.
 NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds.
 NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.
 15 NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.
 NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.
 NT2RP3003500//SCY1 PROTEIN.
 NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.
 NT2RP3004348//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.
 20 NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).
 NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.
 NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).
 NT2RP4000528//NPL4 PROTEIN.
 NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds.
 25 NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds.
 NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.
 NT2RP4001207//Homo sapiens Ran binding protein 11 mRNA, complete cds.
 NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).
 NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.
 30 NT2RP4001339//Homo sapiens mRNA for AMMERC1 protein.
 NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.
 NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.
 NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds.
 35 NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).
 OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.
 OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).
 OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.
 OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857O7
 40 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).
 OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.
 OVARC1001555//NGG1-INTERACTING FACTOR 3.
 OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).
 OVARG1001943//Mus musculus DEBT-91 mRNA, complete cds.
 45 PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.
 PLACE1000066//SSU72 PROTEIN.
 PLACE1000610//MSN5 PROTEIN.
 PLACE1000636//MALE STERILITY PROTEIN 2.
 PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.
 50 PLACE1000987//Rattus norvegicus late gestation lung 2 protein (Lgl2) mRNA, complete cds.
 PLACE1001036//Homo sapiens mRNA for alpha integrin binding protein 63, partial.
 PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.
 PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.
 PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.
 55 PLACE1003602//Homo sapiens mRNA expressed in placenta.
 PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.
 PLACE1004256//Mus musculus short coiled coil protein SCOCO (Scoc) mRNA, complete cds.
 PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds.

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PLACE1004866//MALE STERILITY PROTEIN 2.
 PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds
 PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.
 PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).
 5 PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.
 PLACE1005187//APAG PROTEIN.
 PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds.
 PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds.
 PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds.
 10 PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA, partial cds.
 PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.
 PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds.
 PLACE1007105//Homo sapiens muskelin (MKLN1) mRNA, complete cds.
 PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.
 15 PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.
 PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.
 PLACE1007897//Homo sapiens FLASH mRNA, complete cds.
 PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.
 PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).
 20 PLACE1008398//GENE 33 POLYPEPTIDE.
 PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).
 PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.
 PLACE1009020//NIFS PROTEIN.
 PLACE1009060//BRO1 PROTEIN.
 25 PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.
 PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds.
 PLACE1009571//Homo sapiens PTD002 mRNA, complete cds.
 PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.
 PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).
 30 PLACE1010261//SEGREGATION DISTORTER PROTEIN.
 PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
 PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.
 PLACE1010579//Homo sapiens CED-6 protein (CED-6) mRNA, complete cds.
 PLACE1010628//Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and
 35 S171 gene, partial cds.
 PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.
 PLACE1010761//Homo sapiens mRNA for cisplatin resistance-associated overexpressed protein, complete cds.
 PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB.
 PLACE1011340//Homo sapiens IDN3-B mRNA, complete cds.
 40 PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds.
 PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).
 PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds.
 PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds.
 THYRO1000173//Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.
 45 THYRO1000401//Human TcD37 homolog (HTcD37) mRNA, partial cds.
 THYRO1000666//Mus musculus mRNA for kinesin like protein 9.
 THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.
 THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.
 THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.
 50 THYRO1001703//NIFR3-LIKE PROTEIN.
 THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).
 Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1 (AIPL1) gene, complete cds.
 Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.
 Y79AA1000268//Mus musculus Nip2l mRNA, complete cds.
 55 Y79AA1000313//CALPHOTIN.
 Y79AA1000540//CELL POLARITY PROTEIN TEA1.
 Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.
 Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds.

Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.

Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.

Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.

Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds. Y79AA1002083//H. sapiens mRNA for MUF1 protein.

Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.

Y79AA1002311//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.

Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

[0292] Among the clones other than the above-mentioned, there were 36 clones that were similarly classified into the functional categories based on the results of functional domain search using the Pfam program. These clones were categorized as follows.

[0293] Clones presumably belonging to the category of secretory or membrane proteins are two clones, MAMMA1002498 and NT2RM4002287; a clone presumably belonging to the category of glycoproteins-associated proteins is a clone MAMMA1002498; clones presumably belonging to the category of signal transduction-associated proteins are 11 clones, HEMBA1001247, NT2RM2001813, NT2RM4001454, NT2RP2005140, NT2RP2005293, NT2RP3000487, NT2RP3003311, PLACE1000972, PLACE1003723, PLACE1005327, and PLACE3000124; clones presumably belonging to the category of transcription-associated proteins are 12 clones, HEMBA1003257, NT2RM2000101, NT2RM2001797, NT2RP1000101, NT2RP2002208, NT2RP3001214, NT2RP3003278, NT2RP4001235, PLACE1000050, PLACE1001716, PLACE1002499, and PLACE1007544; clones presumably belonging to the category of enzymes and/or metabolism-associated proteins are 2 clones, HEMBA1005732 and MAMMA1000402; clones presumably belonging to the category of DNA- and/or RNA-binding proteins are 4 clones, HEMBA1004596, OVARC1000148, PLACE1003334, and THYRO1001661; a clone presumably belonging to the category of protein synthesis- and/or protein transport-associated proteins is a clone, HEMBA1006284.

[0294] So far, useful information for presuming the functions is unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

[0295] So far, useful information for presuming the functions is unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

HEMBA1000042,	HEMBA1000046,	HEMBA1000050,	HEMBA1000076,	HEMBA1000193,	HEMBA1000213,
HEMBA1000227,	HEMBA1000231,	HEMBA1000243,	HEMBA1000244,	HEMBA1000251,	HEMBA1000264,
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HEMBA1000338,	HEMBA1000351,	HEMBA1000357,	HEMBA1000376,	HEMBA1000387,	HEMBA1000392,
HEMBA1000396,	HEMBA1000428,	HEMBA1000442,	HEMBA1000456,	HEMBA1000459,	HEMBA1000460,
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	HEMBA1002328,	HEMBA1002337,	HEMBA1002348,	HEMBA1002349,	HEMBA1002381,	HEMBA1002430,
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15	HEMBB1000402,	HEMBB1000420,	HEMBB1000434,	HEMBB1000438,	HEMBB1000441,	HEMBB1000449,
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	MAMMA1001635,	MAMMA1001649,	MAMMA1001663,	MAMMA1001670,	MAMMA1001671,	MAMMA1001683,
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	MAMMA1001818,	MAMMA1001824,	MAMMA1001848,	MAMMA1001851,	MAMMA1001854,	MAMMA1001858,
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20	MAMMA1002033,	MAMMA1002041,	MAMMA1002042,	MAMMA1002047,	MAMMA1002056,	MAMMA1002058,
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40	Y79AA1001281,	Y79AA1001511,	Y79AA1001541,	Y79AA1001555,	Y79AA1001585,	Y79AA1001665,
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	NT2RP2002070,					

45 Homology Search Result Data 1.

[0296] The result of the homology search of the SwissProt using the 5'-end sequence.

[0297] Data include

50 the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the organism and the Accession No. of the top hit data, as in the order separated by //.

55 [0298] Data are not shown for the clones in which the P-value was higher than 1.

[0299] The P-value is a score obtained statistically by taking into account the possible similarity between two sequences. In general, the smaller P-value reflects the higher similarity. (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. &

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States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

5 F-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.8e-85:244:75//MUS MUSCULUS (MOUSE)//Q61712
 F-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINETRNA LIGASE)
 (LEURS)//7.6e-57:231:53//CAENORHABDITIS ELEGANS//Q09996
 F-HEMBA1000020//TUBULIN BETA CHAIN.//1.0e-92:143:80//AJELLOMYCES CAPSULATA (HISTOPLASMA
 CAPSULATUM)//P41742
 10 F-HEMBA1000030//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)//0.021:136:33//PLASMODIUM
 KNOWLESI (STRAIN NURI)//P04922
 F-HEMBA1000042//METALLOTHIONEIN 10-II (MT-10-II)//0.71:64:32//MYTILUS EDULIS (BLUE MUSSEL)//
 P80247
 F-HEMBA1000046//PROTEIN Q300.//0.92:40:37//MUS MUSCULUS (MOUSE)//Q02722
 F-HEMBA1000050//COMPETENCE PROTEIN S.//0.50:28:35//BACILLUS SUBTILIS//P80355
 15 F-HEMBA1000076//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34)//0.86:41:41//HOMO SAPIENS
 (HUMAN)//P56385
 F-HEMBA1000111
 F-HEMBA1000129//UVSW PROTEIN (DAR PROTEIN)//0.023:68:33//BACTERIOPHAGE T4//P20703
 F-HEMBA1000141//YSY6 PROTEIN.//0.90:29:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//
 20 P38374
 F-HEMBA1000150//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.4e-16:47:70//HOMO SAPIENS (HUMAN)//
 P39193
 F-HEMBA1000156//IMMEDIATE-EARLY PROTEIN.//8.1e-07:143:28//HERPESVIRUS SAIMIRI (STRAIN 11)//
 Q01042
 25 F-HEMBA1000158//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT)//7.9e-11:129:40//HOMO SAPIENS
 (HUMAN)//Q93074
 F-HEMBA1000168//INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS)//0.00055:86:36//MUS MUSCULUS
 (MOUSE)//P81122
 F-HEMBA1000180//VPU PROTEIN (U ORF PROTEIN)//0.22:73:28//CHIMPANZEE IMMUNODEFICIENCY VI-
 30 RUS (SIV(CPZ)) (CIV)//P17286
 F-HEMBA1000185//RAS-1 PROTEIN.//5.1e-10:121:29//NEUROSPORA CRASSA//P22126
 F-HEMBA1000193//PROLINE-RICH PEPTIDE P-B.//0.00078:56:41//HOMO SAPIENS (HUMAN)//P02814
 F-HEMBA1000201//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.00061:49:42//MUS MUSCULUS
 (MOUSE)//P05142
 35 F-HEMBA1000213
 F-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PRO-
 TEIN).//1.6e-59:115:53//MUS MUSCULUS (MOUSE)//Q61221
 F-HEMBA1000227//SUPPRESSOR PROTEIN SRP40.//0.00059:135:22//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST)//P32583
 40 F-HEMBA1000231//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//0.024:60:38//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)//Q10264
 F-HEMBA1000243//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0038:125:34//HOMO SAPIENS (HU-
 MAN)//P08547
 F-HEMBA1000244//HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC REGION.//3.1e-17:
 45 149:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)//P40480
 F-HEMBA1000251
 F-HEMBA1000264//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552
 F-HEMBA1000280//SHORT NEUROTOXIN 1 (TOXIN C-6).//0.98:58:31//NAJA NAJA KAOUTHIA (MONOCLED
 COBRA) (NAJA NAJA SIAMENSIS)//P14613
 50 F-HEMBA1000282//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.14:26:65//HOMO SAPIENS (HUMAN)//
 P39188
 F-HEMBA1000288
 F-HEMBA1000290//HYPOTHETICAL 14 KD PROTEIN IN TVRI-6 REPETITIVE REGION.//3.8e-06:98:39//HOMO
 SAPIENS (HUMAN)//P10516
 55 F-HEMBA1000302
 F-HEMBA1000303//HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME III.//1.3e-05:69:42//
 CAENORHABDITIS ELEGANS//Q03601
 F-HEMBA1000304//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.021:18:83//HOMO SAPIENS (HUMAN)//

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F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E4.4 IN CHROMOSOME III.//0.90:94:25//CAENORHABDITIS ELEGANS.//P34343
 F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B).//0.76:41:41//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531
 5 F-NT2RP4000996//PROTEIN Q300.//0.00024:41:53//MUS MUSCULUS (MOUSE).//Q02722
 F-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.7e-115:261:82//RATTUS NORVEGICUS (RAT).//O54888
 10 F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.50:61:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42377
 F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR.//0.010:152:29//BACILLUS SUBTILIS.//P50840
 F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.9e-05:247:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
 15 F-NT2RP4001029//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.1e-14:175:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002
 F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//1.5e-74:272:55//CAENORHABDITIS ELEGANS.//Q09996
 20 F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//0.0064:76:38//CAENORHABDITIS ELEGANS.//P34664
 F-NT2RP4001064//DUALIN.//2.5e-24:199:38//GALLUS GALLUS (CHICKEN).//Q90830
 F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.11:139:38//HOMO SAPIENS (HUMAN).//O00268
 25 F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.5e-22:242:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P13586
 F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I).//1.7e-82:178:69//SUS SCROFA (PIG).//Q29099
 30 F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN.//0.00039:141:26//RATTUS NORVEGICUS (RAT).//P49911
 F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//9.9e-07:79:43//HOMO SAPIENS (HUMAN).//P78563
 F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.4e-16:207:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
 35 F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.1e-115:224:99//RATTUS NORVEGICUS (RAT).//P38378
 F-NT2RP4001122//TIPD PROTEIN.//7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//O15736
 F-NT2RP4001126//TRICHOHYALIN.//1.4e-19:257:28//OVIS ARIES (SHEEP).//P22793
 40 F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-).//0.00010:204:25//METHANOCOCCUS JANNASCHII.//Q58896
 F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION.//4.5e-34:168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616
 F-NT2RP4001148//SOF1 PROTEIN.//2.4e-41:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33750
 45 F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//1.3e-08:106:41//VOLVOX CARTERI.//P21997
 F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.6e-24:194:32//GALLUS GALLUS (CHICKEN).//P35331
 50 F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0056:117:25//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
 F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER).//P52178
 F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0029:117:26//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
 55 F-NT2RP4001207//CHROMOSOME SEGREGATION PROTEIN CSE1.//1.0e-07:144:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33307
 F-NT2RP4001210//DERMORPHIN 1 PRECURSOR [CONTAINS: DELTORPHIN (DERMENKEPHALIN); DER-

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F-Y79AA1001875//CTT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654
F-Y79AA1001923//H.sapiens CpG island DNA genomic MseI fragment, clone 193c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186
5 F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184
F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340
10 F-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 526114, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214
F-Y79AA1002089
F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548
F-Y79AA1002103//HS_3052_B1_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014
15 F-Y79AA1002115
F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693
F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358
20 F-Y79AA1002204//HS_2235_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260
F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397
F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719
25 F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615
F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043
F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738
30 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045
F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592
F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015
35 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555
F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886
F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534
F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877
F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101
40 F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208
F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.0e-159:411:100//AC005920
F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//1.1e-118:609:84//AC004662
45 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//4.4e-90:529:88//U49385
F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196
F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917
50 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116
F-Y79AA1002482//Homo sapiens full-length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022
F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

55 Homology Search Result Data 3.

[0303] The result of the homology search of the GenBank using the clone sequence of 3'-end except EST and STS.
[0304] Data include

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CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//3.8e-07:421:59//AF030694

R-NT2RP4000997//Homo sapiens chromosome 17, clone 104H12, complete sequence.//4.2e-37:499:72//AC000003

R-NT2RP4001004//HS_3163_A2_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=4 Row=O, genomic survey sequence //2.8e-38:241:90//AQ168515

R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.
7.1e-55:372:73//AC006023

R-NT2RP4001010//Homo sapiens full-length insert cDNA clone ZD38E12.//3.3e-09:153:74//AF086247

R-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.1e-34:361:78//U20086

R-NT2RP4001041//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//9.9e-84:435:96//AC005216

R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds.//6.2e-50:282:94//AB007859

R-NT2RP4001064//H.sapiens NOS2 gene, exon 15.//0.71:183:61//X85771

R-NT2RP4001078//Human D-site binding protein gene, exon 4 and complete cds.//1.9e-114:569:97//U48213

R-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase, partial.//2.4e-118:574:98//AJ010953

R-NT2RP4001080//Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence.//0.013:430:58//AE001429

R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 protein, partial cds.//1.8e-119:548:95//AB011164

R-NT2RP4001095//Homo sapiens cosmid clones IM0525, LC1233, Qc3C1, LB1439, Qc12C11 and 220B3 from Xq28, complete sequence.//2.8e-39:312:81//AF003626

R-NT2RP4001100//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS//8.7e-41:389:78//Z78021

R-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//2.8e-12;292:68//M96629

R-NT2RP4001122//Caenorhabditis elegans cosmid F44D12, complete sequence.//0.97:129:66//Z68298

R-NT2RP4001126//HS_3146_A1_805_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=9 Row=C, genomic survey sequence//0.013:268:63//AQ141093

R-NT2RP4001138

R-NT2RP4001143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING
DRAFT SEQUENCE//1.8e-31:380:68//AL031668

R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-83:325:92//AC005095

R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//8.1e-32:553:67//D67067

R-NT2RP4001150//AK011 Genomic DNA *Hordeum vulgare* genomic clone tel44a similar to barley TAS, genomic survey sequence.//0.91:132:63//AQ248412

R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence.//4.0e-118:437:97//AB003468

R-NT2RP4001174//Homo sapiens 12q24 BAC RPC11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//1.7e-33:289:82//AC002996

R-nnnnnnnnnnnnnnn//P.falciparum mRNA for AARP2 protein.//0.93:187:64//Y08924

R-NT2RP4001207

R-NT2RP4001210//CIT-HSP-2042D13.TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence.//3.8e-06:268:63//B74772

R-NT2RP4001213//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//4.7e-16:371:66//M99593

R-NT2RP4001219//HS_2190_A1_A06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence//2 4e-06:288:61//AQ216635

R-NT2RP4001228//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING
DRAFT SEQUENCE//0.024:357:58//AL031745

R-NT2RP4001235//HS_3047_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=L. genomic survey sequence//0.0033;301.63//AQ126918

R-NT2RP4001256//HS_3007_A2_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence.//1.5e-11:140:80//AQ118389

R-NT2RP4001260//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//0.0013:486:59//AE001426

R-NT2RP4001274//RPCI11-24O21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24O21, genomic survey sequence.//3.9e-25:142:99//AQ013887

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R-Y79AA1002211//H.sapiens NGAL gene//1.0:311:59//X99133
R-Y79AA1002220//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING
DRAFT SEQUENCE//5.9e-07:535:57//AL034557
R-Y79AA1002229
5 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//6.1e-117:564:98//AB014592
R-Y79AA1002246
R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds//1.3e-92:453:97//AB013384
R-Y79AA1002298//HS_3071_B2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens ge-
nomic clone Plate=3071 Col=16 Row=J, genomic survey sequence//1.9e-56:384:87//AQ171331
10 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.5e-108:403:99//AB014534
R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-117312 map 10q25, complete sequence//
1.1e-07:368:61//AC005887
R-Y79AA1002351
R-Y79AA1002361//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65b9, reverse read cpg65b9.rt1a//
15 0.57:59:79//Z62206
R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence//2.0e-98:385:99//
AC005920
R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence//5.4e-59:490:
76//AC004662
20 R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete se-
quence//6.3e-08:103:80//AC004087
R-Y79AA1002431
R-nnnnnnnnnnnn//Mouse transcriptional control element//0.064:84:71//M17284
R-Y79AA1002472//Homo sapiens chromosome 19, BAC CTY-B-393i15 (BC301323), complete sequence//1.6e-
25 103:525:96//AC006116
R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence//9.7e-38:302:
83//AC006238
R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B)//0.23:266:61//X95276

30 Homology Search Result Data 4.

[0307] The result of the homology search of the Human Unigene using the clone sequence of 5'-end.

[0308] Data include

35 the name of clone,
title of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

40 [0309] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069
F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:
L40157
45 F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668
F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078
F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247
F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharo-
myces cerevisiae]//0.00019:192:65//Hs.7900:W22411
50 F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759
F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910
F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734
F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:
342:61//Hs.14207:U86453
55 F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8e-169:791:98//Hs.27197:
AB018340
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200
F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//

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F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503
F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//
Hs.24812:AF069532
F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371
5 F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542
F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888
F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058
F-NT2RP4000979
F-NT2RP4000984
10 F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913
F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068
F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204
F-NT2RP4001004
F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718
15 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.
113287:AF009204
F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494
F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:
L40157
20 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157
F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481:
AJ006470
F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497
F-NT2RP4001079//Homo sapiens mRNA for putative Ca²⁺-transporting ATPase, partial//1.4e-131:634:98//Hs.
25 106778:AJ010953
F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//0.025:166:66//Hs.
146459:X66975
F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164
F-NT2RP4001095
30 F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.4e-93:448:98//Hs.105837:AA536054
F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis
familiaris]//2.2e-26:171:92//Hs.14038:R06800
F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142
F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//5.8e-37:185:
35 100//Hs.126925:AA931237
F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.1433 82:AA476266
F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI358261
F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207
F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171
40 F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59//Hs.2998:X67734
F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324
F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264
F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324
F-NT2RP4001207
45 F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI017636
F-NT2RP4001213//KRAB zinc finger protein {alternative products}//1.1e-45:187:74//Hs.22556:U37251
F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262
F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.
122967:AF059569
50 F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778
F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463
F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A1, 59kD, acidic component)//0.015:246:62//
Hs.31121:U40571
F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578
55 F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736
F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding
mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250
F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI375917

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F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533
 F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142:90//Hs.103349:AI141124
 F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:67//Hs.104115:X52332
 F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62//Hs.106387:AF029778
 5 F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173
 F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs.78501:L13720
 F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382
 F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611
 10 F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943
 F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348:88//Hs.18122:AI338045
 F-Y79AA1002093
 F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865
 F-Y79AA1002115
 15 F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395
 F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165:90//Hs.6473:AA853955
 F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393:62//Hs.77864:AB014538
 F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515
 F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldoteanax]//2.3e-113:568:
 20 96//Hs.111637:AA305890
 F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338:73//Hs.26662:U55984
 F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477
 F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:63//Hs.1560:D42045
 25 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821:98//Hs.100729:AB014592
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731:AB014555
 30 F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622:97//Hs.30898:AB014534
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999
 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete
 35 cds//0.028:587:58//Hs.2363:L36069
 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377
 F-Y79AA1002399
 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569
 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142
 40 F-Y79AA1002431
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302
 45

Homology Search Result Data 5.

[0310] The result of the homology search of the Human Unigene using the clone sequence of 3'-end.

[0311] Data include

the name of clone,
 title of the top hit data,
 the P-value: the length of the compared sequence: identity (%), and
 the Accession No. of the top hit data, as in the order separated by //.

[0312] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0313] Data are not shown for the clones in which the P-value was higher than 1.

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R-HEMBA1000005//ESTs, Highly similar to HYPOTHETICAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME III [Caenorhabditis elegans]//5.6e-93:501:93//Hs.13015:AA628434
R-HEMBA1000030//Human POU domain protein (Brm-3b) mRNA, complete cds//0.83:314:61//Hs.266:U06233
R-HEMBA1000042//Archain//1.4e-45:282:89//Hs.33642:X81198
5 R-HEMBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-52:528:72//Hs.154326:D42087
R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243340
R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329
R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788
R-HEMBA1000129//ESTs, Weakly similar to contains similarity to helicases [C.elegans]//4.4e-90:502:90//Hs.
10 55918:AA151667
R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.1e-100:514:94//Hs.27197:AB018340
R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-45:435:77//Hs.153026:AB014540
15 R-nnnnnnnnnnnn//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]//7.7e-92:428:100//Hs.126925:AA931237
R-HEMBA1000158
R-nnnnnnnnnnnn//ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58:91//Hs.5570:AI377863
R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545
20 R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366
R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927
R-HEMBA1000201//Human Ini1 mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847
R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311
R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532
25 R-nnnnnnnnnnnn//EST//2.2e-100:498:96//Hs.161570:W80404
R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70//Hs.127649:AB007874
R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276:75//Hs.5737:AB007944
R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019
30 R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808
R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424
R-nnnnnnnnnnnn//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.9e-14:208:73//Hs.93332:AA811920
R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485
35 R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962
R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409
R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122:67//Hs.129748:AB011099
R-nnnnnnnnnnnn//ESTs//7.4e-76:386:97//Hs.22276:AA191323
R-nnnnnnnnnnnn//Human Ca²⁺-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160:98//
40 Hs.151301:U36448
R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e-103:489:99//Hs.108881:AI018024
R-nnnnnnnnnnnn//ESTs//9.3e-99:472:98//Hs.163512:AA903238
R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560
R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//
45 Hs.73614:U83460
R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243
R-HEMBA1000357//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:K00629
R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857
50 R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938
R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960
R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//
Hs.73614:U83460
R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878
55 R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:AI340248
R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]//1.1e-44:447:75//Hs.42849:N31920
R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//6.1e-92:373:99//Hs.48675:AI005282

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R-nnnnnnnnnnnnn//ESTs//1.7e-55:478:76//Hs.154554:AA552715
R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs.
50441:AA747428
R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349
5 R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]//
6.5e-86:518:90//Hs.25682:AA857843
R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274
R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977
R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:
10 AB014592
R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME [D.melanogaster]//9.0e-102:
507:96//Hs.25895:AI341537
R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555
R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288
15 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:
AB014534
R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985
R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371
R-Y79AA1002361
20 R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908
R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000
R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753
R-Y79AA100243//EST//6.6e-23:128:98//Hs.128417:AA975026
R-nnnnnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 68 [Saccharomyces cerevisiae]
25 //4.4e-62:390:88//Hs.143930:AI207821
R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870
R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788
R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

Homology Search Result Data 6

[0314] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1 //1.9E-250//554aa//85%//Q61712
C-HEMBA1000030
40 C-HEMBA1000046
C-HEMBA1000050
C-HEMBA1000076
C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M) //1.9E-12//368aa//24%//P08553
45 C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3-GAMMA (HNF-3G) //5E-16//166aa//36%//P35584
C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) //2.9E-14//303aa//25%//P35662
C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A //3.4E-12//125aa//31%//P48555
C-HEMBA1000193
C-HEMBA1000227
50 C-HEMBA1000288
C-HEMBA1000302
C-HEMBA1000304
C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1 //5.2E-49//107aa//91 %//035594
55 C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083) //0//1950bp//98%//AL049654
C-HEMBA1000387
C-HEMBA1000392

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C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0//3574bp//99%//AB023229
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//
 0.000000032//67aa//31%//P53915
 C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0//1927bp//99%//AB007939
 5 C-NT2RP4000833
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-94//810bp//65%//Y18265
 C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.5E-21//271 aa//28%//Q00808
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE)(ARGININE AMI-
 NOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV)(AP-B).//5.7E-82//324aa//48%//O09175
 10 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//55%//P16415
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%//O35682
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96//513aa//42%//P22314
 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26//
 227aa//36%//Q06828
 15 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THI-
 OLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING EN-
 ZYME 1).//1.5E-76//346aa//43%//Q61068
 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%//Y16521
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.00000014//185aa//25%//Q58900
 20 C-NT2RP4000955
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//
 90aa//42%//P38660
 C-NT2RP4000975
 C-NT2RP4000979
 25 C-NT2RP4000984
 C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%//P34579
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE 1135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA
 POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87%//P70700
 C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%//P39968
 30 C-NT2RP4001006
 C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete cds.//0//2482bp//99%//AB023181
 C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE).//1.5E-
 92//443aa//44%//Q09996
 C-NT2RP4001057
 35 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%//Q64375
 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.3E-123//
 563aa//46%//P13586
 C-NT2RP4001080//Homo sapiens mRNA for Rodi, complete cds.//0//1439bp//99%//AB023967
 C-NT2RP4001086
 40 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAM-
 INASE) (RNA EDITING ENZYME 1).//2.6E-17//121aa//36%//P51400
 C-NT2RP4001100
 C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%//
 P38378
 45 C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%//O15736
 C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%//Q07283
 C-NT2RP4001138
 C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (EC 3.5.1.18) (SDAP).//0.00000021//
 93aa//33%//P44514
 50 C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%//P33750
 C-NT2RP4001149
 C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//
 3.4E-29//385aa//29%//P35331
 C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
 55 4.7E-29//227aa//35%//P52178
 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.4E-104//1460bp//
 65 %//U95760
 C-NT2RP4001207

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F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT).//7.4e-38//136//41//P51003
 F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.0e-08//180//28//P32323
 F-NT2RP2005882
 5 F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.0022//69//39//P39217
 F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).//0.00035//127//31//P15276
 F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.97//71//28//P05204
 F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).//0.064//110//34//P39881
 10 F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.020//95//29//P15583
 F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.8e-05//165//29//P17437
 15 F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.035//152//30//P10162
 F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VMW118 PROTEIN).//0.38//124//31//P28284
 F-OVARC1001029
 20 F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.45//61//24//Q42377
 F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29).//0.70//121//32//P47845
 F-PLACE1005549//RHO1 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRESSOR SKC1).//3.2e-08//205//24//P53046
 25 F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210).//0.99//52//38//P01668

Homology Search Result Data 8.

30 **[0318]** The result of the homology search of the GenBank using the clone sequence of 5'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

[0319] Data include

35 the name of clone,
 definition of the top hit data,
 the P-value: the length of the compared sequence: identity (%), and
 the Accession No. of the top hit data, as in the order separated by //.

40 **[0320]** Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000497
 F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs.//6.6e-101//473//99//V00710
 F-HEMBA1003854//Homo sapiens clone RG270D13, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces.//1.7e-05//412//61//AC005081
 45 F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence.//0.77//466//59//AC002386
 F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds.//6.7e-07//492//57//U29953
 F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//2.9e-47//341//77//S54641
 50 F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2, complete sequence.//0.28//436//59//Z83851
 F-HEMBA1006092//Human chromosome 16p13.11 BAC clone CIT987SK-29B12 complete sequence.//0.28//309//60//U95738
 F-HEMBA1006406//HS_2268_B2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=14 Row=F, genomic survey sequence.//3.7e-69//340//99//AQ070566
 55 F-HEMBA1006650//H.sapiens CpG island DNA genomic Mse1 fragment, clone 5h5, forward read cpg5h5.f1a.//9.4e-24//143//96//Z55730
 F-HEMBA1006812//X.laevis xUBFalpha mRNA for upstream binding factor 2.//0.96//234//64//X59863

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F-OVARC1000008///0.0040//674//57//M82836
 F-OVARC1000724//Herpes simplex virus type I immediate early (IE) gene 3 for transcriptional activator IE175 (= ICP 4) //1.1e-07//519//59//X06461
 F-OVARC1000751//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//7.2e-11//509//62//AC004221
 F-OVARC1001029//Human DNA sequence from clone 19408 on chromosome 6q24.1-25.3 Contains STS and GSSs, complete sequence.//1.1e-05//388//61//AL031769
 F-PLACE1000814//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//1.4e-84//717//78//AC002427
 F-PLACE1003030
 F-PLACE1005549//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//4.9e-56//709//68//U02081
 F-PLACE1007218//Homo sapiens chromosome 20 clone RP3-387E22, *** SEQUENCING IN PROGRESS ***, in unordered pieces.//3.1e-39//214//98//AL031660

Homology Search Result Data 9.

[0321] The result of the homology search of the GenBank using the clone sequence of 3'-end (54 clones selected in EXAMPLE 16.) except EST and STS.

[0322] Data include

the name of clone,
 definition of the top hit data,
 the P-value: the length of the compared sequence: identity (%), and
 the Accession No. of the top hit data, as in the order separated by //.

[0323] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0324] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000497//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.4e-38//185//84//U14567
 R-HEMBA1001750//Hansenula wingei mitochondrial DNA, complete sequence.//1.7e-07//399//59//D31785
 R-HEMBA1003854//Human DNA sequence from clone 224A6 on chromosome 1p35.1-36.23 Contains part of a gene similar to Mouse Wnt-4 protein, the gene for CDC42 (cell division cycle 42 (GTP-binding protein, 25kD)), ESTs, STSs, GSSs and a CpG Island, complete sequence.//1.4e-75//309//85//AL031281
 R-HEMBA1004193//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-34//188//81//U14567
 R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPCI3-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-06//239//66//AC004241
 R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPCIP704E14135Q2, complete sequence.//3.1e-21//341//67//AJ010598
 R-HEMBA1006038//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//1.7e-24//307//71//AC004678
 R-HEMBA1006092//H.Sapiens mRNA for alpha2-subunit of soluble guanylyl cyclase.//0.76//246//62//X63282
 R-HEMBA1006406//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4 Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.3e-31//297//77//AL023574
 R-HEMBA1006650//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.8e-15//350//65//AC003071
 R-HEMBA1006812//Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCING IN PROGRESS ***, in unordered pieces.//1.8e-55//430//81//Z82207
 R-HEMBA1006722//Homo sapiens clone UWGC:y54c283 from 6p21, complete sequence.//9.1e-39//437//71//AC006166
 R-HEMBA1001197//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.5e-37//275//85//AC004593
 R-HEMBA1001871//Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.//0.00097//410//59//AC004688
 R-MAMMA1001252//Homo sapiens clone 201104, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.//2.9e-13//364//64//AC004529
 R-MAMMA1002094//HS_3163_A1_A09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=17 Row=A, genomic survey sequence.//5.9e-41//256//91//AQ141441

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AMINYLTRANSFERASE) (GALNAC-T1).//1.70E-84//313aa//48%//Q07537
 C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.80E-91//209aa//41%//P52740
 C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.//3.4e-310//1430bp//98%//AF077049
 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gc1) mRNA, complete cds.//1.40E-78//
 227aa//40%//Q01820
 C-Y79AA1001705//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//3.40E-
 47//626bp//68%//AF033120
 C-Y79AA1001711//Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds.//1.20E-258//1185bp//99%//
 J04137
 C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.//
 0//1689bp//98%//AF177145
 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//
 AF192913
 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTI-
 15 VATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489
 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149
 C-Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds.//7.10E-52//279bp//97%//
 AF174602
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE
 20 SPAC10F6.02C.//1.00E-10//94aa//47%//O42643
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743
 C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5.00E-163//752bp//99%//X86018
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415
 25 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133
 C-Y79AA1002204//COMPLEXIN 2 (SYNAPHIN 1) (921-L).//7.50E-09//131aa//35%//Q13329
 C-Y79AA1002208//ANKYRIN.//8.10E-34//188aa//38%//Q02357
 C-Y79AA1002209//TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//1.60E-
 72//437aa//39%//P00952
 30 C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
 TEIN).//0.0000018//140aa//25%//Q13829
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//
 146aa//35%//O16264
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620
 35 C-Y79AA1002246//SYNAPTOTAGMIN V.//1.60E-28//286aa//32%//O00445
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384
 C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.//0//1209bp//99%//AF116574
 C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.90E-186//1130bp//82%//
 X67877
 40 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//
 Y18208
 C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879
 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//
 86%//U49385
 45 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725
 C-Y79AA1002433//Homo sapiens chromatin- specific transcription elongation factor FACT 140 kDa subunit mR-
 NA, complete cds.//0//1545bp//96%//AF152961
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.50E-136//472aa//
 49%//Q05481
 50 C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//
 51%//Q05481
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-311//
 1444bp//98%//AF129534

Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set

forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides.
3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from the group consisting of:

SEQ ID NO: 1 / SEQ ID NO: 5548, SEQ ID NO: 4 / SEQ ID NO: 5549, SEQ ID NO: 5 / SEQ ID NO: 5550, SEQ ID NO: 6 / SEQ ID NO: 5551, SEQ ID NO: 7 / SEQ ID NO: 5552, SEQ ID NO: 8 / SEQ ID NO: 5553, SEQ ID NO: 9 / SEQ ID NO: 5554, SEQ ID NO: 10 / SEQ ID NO: 5555, SEQ ID NO: 11 / SEQ ID NO: 5556, SEQ ID NO: 12 / SEQ ID NO: 5557, SEQ ID NO: 13 / SEQ ID NO: 5558, SEQ ID NO: 14 / SEQ ID NO: 5559, SEQ ID NO: 15 / SEQ ID NO: 5560, SEQ ID NO: 16 / SEQ ID NO: 5561, SEQ ID NO: 17 / SEQ ID NO: 5562, SEQ ID NO: 18 / SEQ ID NO: 5563, SEQ ID NO: 19 / SEQ ID NO: 5564, SEQ ID NO: 20 / SEQ ID NO: 5565, SEQ ID NO: 21 / SEQ ID NO: 5566, SEQ ID NO: 22 / SEQ ID NO: 5567, SEQ ID NO: 23 / SEQ ID NO: 5568, SEQ ID NO: 24 / SEQ ID NO: 5569, SEQ ID NO: 25 / SEQ ID NO: 5570, SEQ ID NO: 26 / SEQ ID NO: 5571, SEQ ID NO: 27 / SEQ ID NO: 5572, SEQ ID NO: 28 / SEQ ID NO: 5573, SEQ ID NO: 29 / SEQ ID NO: 5574, SEQ ID NO: 30 / SEQ ID NO: 5575, SEQ ID NO: 31 / SEQ ID NO: 5576, SEQ ID NO: 32 / SEQ ID NO: 5577, SEQ ID NO: 33 / SEQ ID NO: 5578, SEQ ID NO: 34 / SEQ ID NO: 5579, SEQ ID NO: 35 / SEQ ID NO: 5580, SEQ ID NO: 37 / SEQ ID NO: 5581, SEQ ID NO: 38 / SEQ ID NO: 5582, SEQ ID NO: 39 / SEQ ID NO: 5583, SEQ ID NO: 40 / SEQ ID NO: 5584, SEQ ID NO: 42 / SEQ ID NO: 5585, SEQ ID NO: 43 / SEQ ID NO: 5586, SEQ ID NO: 44 / SEQ ID NO: 5587, SEQ ID NO: 45 / SEQ ID NO: 5588, SEQ ID NO: 46 / SEQ ID NO: 5589, SEQ ID NO: 47 / SEQ ID NO: 5590, SEQ ID NO: 48 / SEQ ID NO: 5591, SEQ ID NO: 49 / SEQ ID NO: 5592, SEQ ID NO: 50 / SEQ ID NO: 5593, SEQ ID NO: 51 / SEQ ID NO: 5594, SEQ ID NO: 52 / SEQ ID NO: 5595, SEQ ID NO: 53 / SEQ ID NO: 5596, SEQ ID NO: 54 / SEQ ID NO: 5597, SEQ ID NO: 55 / SEQ ID NO: 5598, SEQ ID NO: 56 / SEQ ID NO: 5599, SEQ ID NO: 57 / SEQ ID NO: 5600, SEQ ID NO: 58 / SEQ ID NO: 5601, SEQ ID NO: 59 / SEQ ID NO: 5602, SEQ ID NO: 60 / SEQ ID NO: 5603, SEQ ID NO: 61 / SEQ ID NO: 5604, SEQ ID NO: 62 / SEQ ID NO: 5605, SEQ ID NO: 63 / SEQ ID NO: 5606, SEQ ID NO: 65 / SEQ ID NO: 5607, SEQ ID NO: 66 / SEQ ID NO: 5608, SEQ ID NO: 67 / SEQ ID NO: 5609, SEQ ID NO: 68 / SEQ ID NO: 5610, SEQ ID NO: 69 / SEQ ID NO: 5611, SEQ ID NO: 70 / SEQ ID NO: 5612, SEQ ID NO: 71 / SEQ ID NO: 5613, SEQ ID NO: 72 / SEQ ID NO: 5614, SEQ ID NO: 74 / SEQ ID NO: 5615, SEQ ID NO: 76 / SEQ ID NO: 5616, SEQ ID NO: 77 / SEQ ID NO: 5617, SEQ ID NO: 78 / SEQ ID NO: 5618, SEQ ID NO: 79 / SEQ ID NO: 5619, SEQ ID NO: 80 / SEQ ID NO: 5620, SEQ ID NO: 81 / SEQ ID NO: 5621, SEQ ID NO: 82 / SEQ ID NO: 5622, SEQ ID NO: 83 / SEQ ID NO: 5623, SEQ ID NO: 84 / SEQ ID NO: 5624, SEQ ID NO: 85 / SEQ ID NO: 5625, SEQ ID NO: 86 / SEQ ID NO: 5626, SEQ ID NO: 87 / SEQ ID NO: 5627, SEQ ID NO: 88 / SEQ ID NO: 5628, SEQ ID NO: 89 / SEQ ID NO: 5629, SEQ ID NO: 90 / SEQ ID NO: 5630, SEQ ID NO: 91 / SEQ ID NO: 5631, SEQ ID NO: 92 / SEQ ID NO: 5632, SEQ ID NO:

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- 5 4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.
5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.
6. A substantially pure protein encoded by polynucleotide of claim 4.
- 10 7. A partial peptide of the protein of claim 6.
8. An isolated polynucleotide selected from the group consisting of
- 15 (a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOs:

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 SEQ ID NO:19008, SEQ ID NO:19010, SEQ ID NO:19015, SEQ ID NO:19017, SEQ ID
 NO:19019, SEQ ID NO:19021, and SEQ ID NO:19023

(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence
 selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted,
 inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino
 acid sequence selected from the amino acid sequences of (b);

(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the
 nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equiv-
 alent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein
 encoded by the polynucleotide of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence
 of (a).

9. A substantially pure protein encoded by the polynucleotide of claim 8.

10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

11. A vector comprising the polynucleotide of claim 5 or 8.
12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
- 5 13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.
- 10 15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.
16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.
- 15 17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.
18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.
19. A method for synthesizing a polynucleotide, the method comprising:
- 20 a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
- b) recovering the synthesized product.
- 25 20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.
21. The method of claim 19, wherein the complementary strand is obtainable by PCR.
22. A method for detecting the polynucleotide of claim 8, the method comprising:
- 30 a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
- b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.
- 35 23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium on which the database is stored.

Figure 1

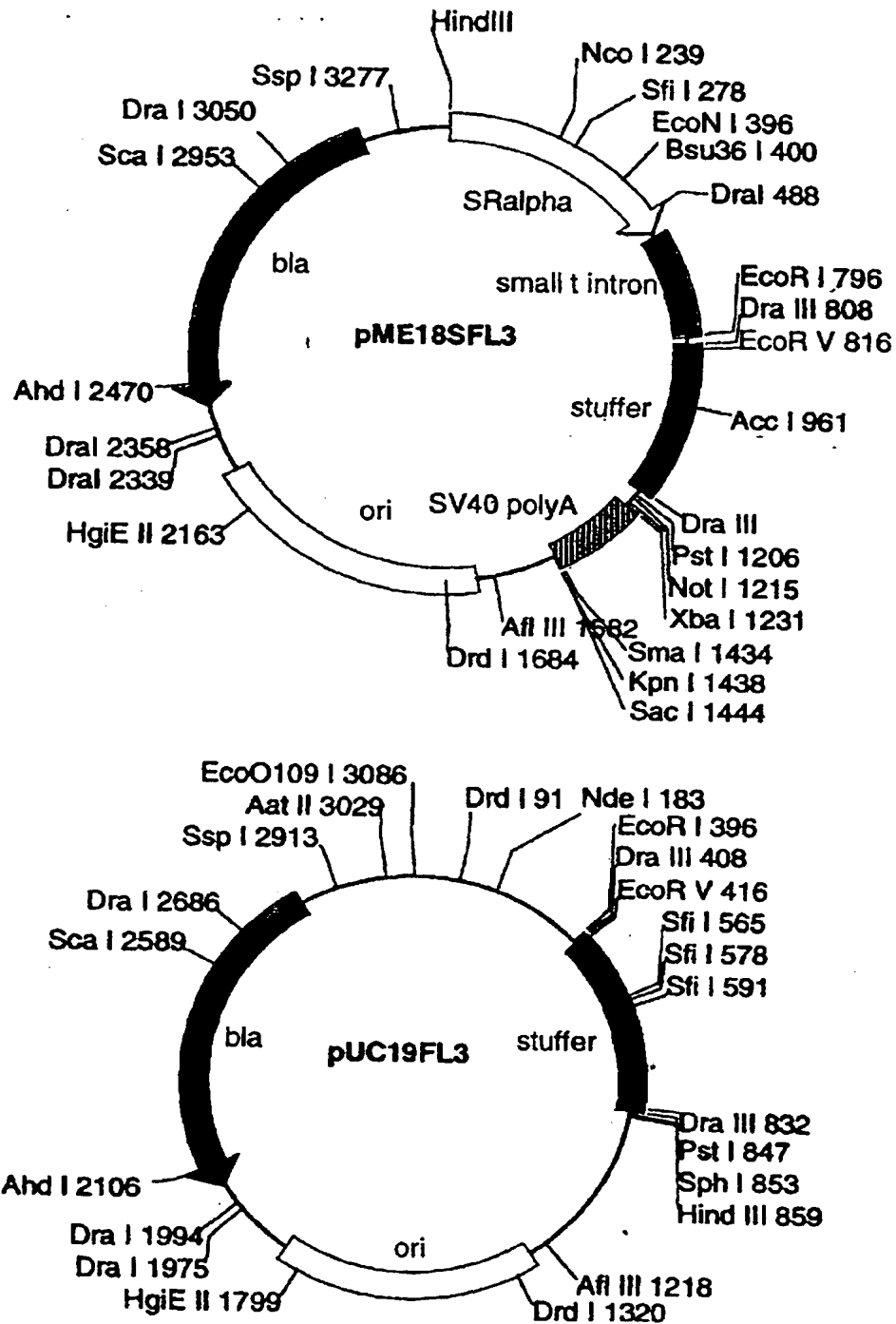


Figure 2

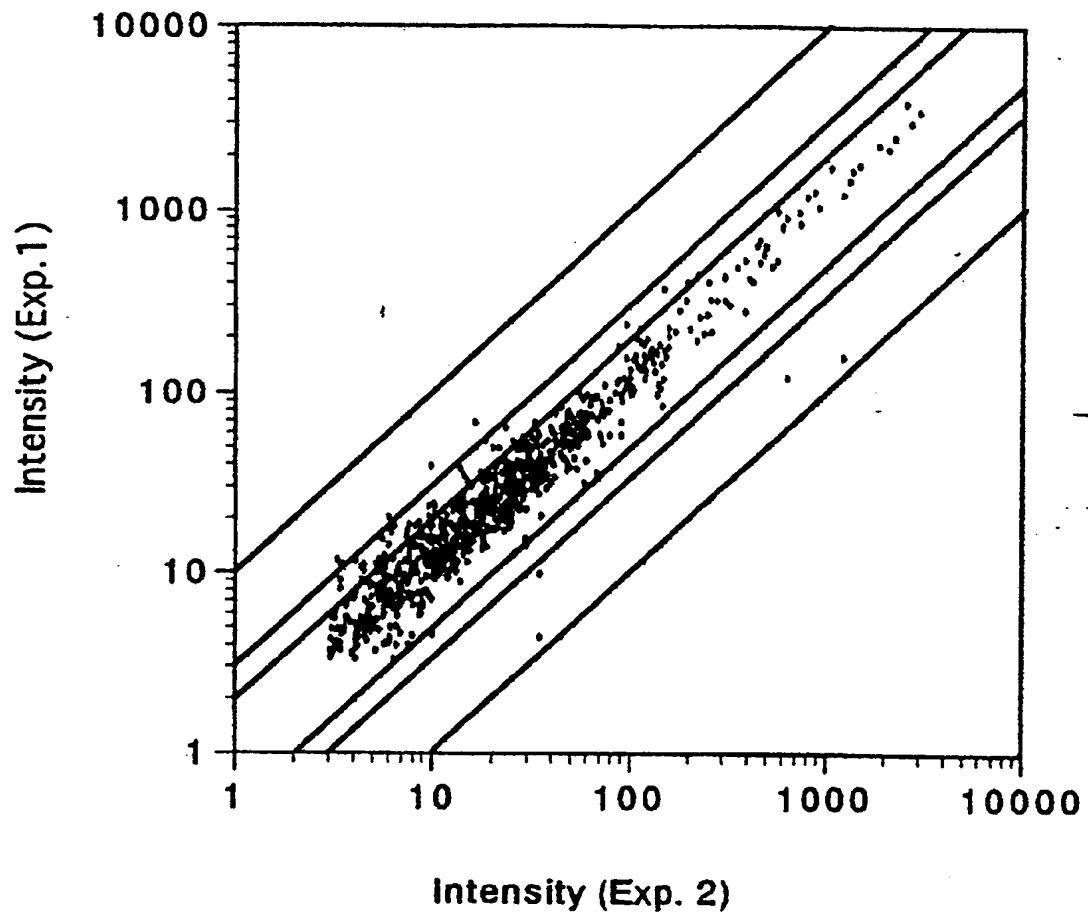


Figure 3

